



Cura 468 SEQ list 0405.txt  
SEQUENCE LISTING

<110> Edinger, Shlomit R  
Gerlach, Valerie  
MacDougall, John R  
Malyankar, Muriel M  
Smithson, Glennnda  
Millet, Isabelle  
Peyman, John A  
Stone, David J  
Gunther, Erik  
Ellerman, Karen  
Shimkets, Richard A  
Padigaru, Muralidhara  
Guo, Xiaojia  
Patturajan, Meera  
Taupier Jr, Raymond J  
Burgess, Catherine E  
Zerhusen, Bryan D  
Kekuda, Ramesh  
Spytek, Kimberly A  
Gangolli, Esha A  
Fernandes, Elma R  
Gorman, Linda

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Phe	His	Met	Asp	Leu	Arg	Thr	Ser	Ser	Ser	Leu	Val	Ala	Pro	Gly	Phe	180	185	190
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Pro	Pro	Glu	Asp	Phe	Cys	Phe	Tyr	Gln	Gly	Ser	Leu	Arg	Ser	His	Arg	210	215	220
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Arg	Ala	Ala	Gln	Cys	Ala	Glu	His	Asn	Ser	Arg	Arg	Phe	Arg	Gly	Arg	260	265	270
His	Tyr	Lys	Trp	Lys	Pro	Tyr	Thr	Gln	Val	Glu	Gln	Asp	Leu	Cys	Lys	275	280	285
Leu	Tyr	Cys	Ile	Ala	Glu	Gly	Phe	Asp	Phe	Phe	Phe	Ser	Leu	Ser	Asn	290	295	300
Lys	Val	Lys	Asp	Gly	Thr	Pro	Cys	Ser	Glu	Asp	Ser	Arg	Asn	Val	Cys	305	310	315
Ile	Asp	Gly	Ile	Cys	Glu	Met	Pro	Gln	Pro	Pro	Lys	Glu	Asp	Leu	Phe	325	330	335
Ile	Leu	Pro	Asp	Glu	Tyr	Lys	Ser	Cys	Leu	Arg	His	Lys	Arg	Ser	Leu	340	345	350
Leu	Arg	Ser	His	Arg	Asn	Glu	Glu	Leu	Asn	Val	Glu	Thr	Leu	Val	Val	355	360	365
Val	Asp	Lys	Lys	Met	Met	Gln	Asn	His	Gly	His	Glu	Asn	Ile	Thr	Thr	370	375	380



## Cura 468 SEQ list 0405.txt

Tyr	Val	Leu	Thr	Ile	Leu	Asn	Met	Val	Ser	Ala	Leu	Phe	Lys	Asp	Gly	385	390	395	400
Thr	Ile	Gly	Gly	Asn	Ile	Asn	Ile	Ala	Ile	Val	Gly	Leu	Ile	Leu	Leu		405	410	415
Glu	Asp	Glu	Gln	Asp	Ile	Cys	Lys	Ala	Leu	Trp	Cys	His	Arg	Ile	Gly		420	425	430
Arg	Lys	Cys	Glu	Thr	Lys	Phe	Met	Pro	Ala	Ala	Glu	Gly	Thr	Ile	Cys		435	440	445
Gly	His	Asp	Met	Trp	Cys	Arg	Gly	Gly	Gln	Cys	Val	Lys	Tyr	Gly	Asp		450	455	460
Glu	Gly	Pro	Lys	Pro	Thr	His	Gly	His	Trp	Ser	Asp	Trp	Ser	Ser	Trp	465	470	475	480
Ser	Pro	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	His	Arg	Ser	Arg		485	490	495
Leu	Cys	Thr	Asn	Pro	Arg	Pro	Ser	His	Gly	Gly	Lys	Phe	Cys	Glu	Gly		500	505	510
Ser	Thr	Arg	Thr	Leu	Lys	Leu	Cys	Asn	Ser	Gln	Lys	Cys	Pro	Arg	Asp		515	520	525
Ser	Val	Asp	Phe	Arg	Ala	Ala	Gln	Cys	Ala	Glu	His	Asn	Ser	Arg	Arg	530	535	540	
Phe	Arg	Gly	Arg	His	Tyr	Lys	Trp	Lys	Pro	Gln	Asp	Leu	Cys	Lys	Leu	545	550	555	560
Tyr	Cys	Ile	Ala	Glu	Gly	Phe	Asp	Phe	Phe	Phe	Ser	Leu	Ser	Asn	Lys		565	570	575
Val	Lys	Asp	Gly	Thr	Pro	Cys	Ser	Glu	Asp	Ser	Arg	Asn	Val	Cys	Ile		580	585	590
Asp	Gly	Ile	Cys	Glu	Gly	Cys	Asp	Asn	Val	Leu	Gly	Ser	Asp	Ala	Val		595	600	605
Glu	Asp	Val	Cys	Gly	Val	Cys	Asn	Gly	Asn	Asn	Ser	Ala	Cys	Thr	Ile	610	615	620	
His	Arg	Gly	Leu	Tyr	Thr	Lys	His	His	His	Thr	Asn	Tyr	Tyr	His	Met	625	630	635	640

Cura 468 SEQ list 0405.txt

Val Thr Ile Pro Ser Gly Ala Arg Ser Ile Arg Ile Tyr Glu Met Asn  
645 650 655

Val Ser Thr Ser Tyr Ile Ser Val Arg Asn Ala Leu Arg Arg Tyr Tyr  
660 665 670

Leu Asn Gly His Trp Thr Val Asp Trp Pro Gly Arg Tyr Lys Phe Ser  
675 680 685

Gly Thr Thr Phe Asp Tyr Arg Arg Ser Tyr Asn Glu Pro Glu Asn Leu  
690 695 700

Ile Ala Thr Gly Pro Thr Asn Glu Thr Leu Ile Val Glu Leu Leu Phe  
705 710 715 720

Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg Leu  
725 730 735

Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala Ile  
740 745 750

Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu Pro  
755 760 765

Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Ser Ala Thr Ala Tyr Ile  
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Ala Leu Ala Phe Leu Glu Ser  
785 790

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<211> 2902

<212> DNA

<213> Homo sapiens

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Cura 468 SEQ list 0405.txt

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 aataacaaat gcaatgcttg gagaatcggc cctggcttca accagaaagt ctaattgtgt 540  
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Cura 468 SEQ list 0405.txt

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cactcgcact ctgaagctct gcaacagtca gaaatgtccc cgggacagtg ttgacttccg 1980
tgctgctcag tgtgccgagc acaacagcag acgattcaga gggcggcact acaagtggaa 2040
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<210> 6  
 <211> 856  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
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## Cura 468 SEQ list 0405.txt

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			20					25					30			
Val	Ser	His	Glu	Ile	Met	His	His	Gln	Arg	Arg	Arg	Arg	Ala	Val	Ala	
		35					40					45				
Val	Ser	Glu	Val	Glu	Pro	Ala	Phe	Leu	Gln	Val	Cys	Arg	Ala	Arg	Glu	
	50					55					60					
Leu	Arg	Leu	Cys	Val	Glu	Ala	Phe	Pro	Ile	Ala	Asn	Ser	Gln	Pro	Gly	
65					70					75					80	
Phe	Leu	Asn	Leu	Ser	Asn	Val	Arg	Ser	His	Trp	Arg	Glu	Gln	His	Ala	
				85					90					95		
Ser	Lys	Arg	Ile	Ile	Thr	Asn	Ala	Met	Leu	Gly	Glu	Ser	Ala	Leu	Ala	
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Ser	Thr	Arg	Lys	Ser	Asn	Cys	Val	Phe	Phe	Leu	Ser	Phe	Tyr	Phe	Phe	
		115					120					125				
Gln	Ser	Gly	Met	Ile	Arg	Thr	Glu	Glu	Ala	Asp	Tyr	Phe	Leu	Arg	Pro	
	130					135					140					
Leu	Pro	Ser	His	Leu	Ser	Trp	Lys	Leu	Gly	Arg	Ala	Ala	Gln	Gly	Ser	
145					150					155					160	
Ser	Pro	Ser	His	Val	Leu	Tyr	Lys	Arg	Glu	Val	Leu	Val	Thr	Ser	Arg	
				165					170					175		
Thr	Trp	Glu	Leu	Ala	His	Gln	Pro	Leu	His	Ser	Ser	Asp	Leu	Arg	Leu	
			180					185					190			
Gly	Leu	Pro	Gln	Lys	Gln	His	Phe	Cys	Gly	Arg	Arg	Lys	Lys	Tyr	Met	
		195					200					205				
Pro	Gln	Pro	Pro	Lys	Glu	Asp	Leu	Phe	Ile	Leu	Pro	Asp	Glu	Tyr	Lys	
	210					215					220					
Ser	Cys	Leu	Arg	His	Lys	Arg	Ser	Leu	Leu	Arg	Ser	His	Arg	Asn	Glu	
225					230					235					240	
Glu	Leu	Asn	Val	Glu	Thr	Leu	Val	Val	Val	Asp	Lys	Lys	Met	Met	Gln	
				245					250					255		
Asn	His	Gly	His	Glu	Asn	Ile	Thr	Thr	Tyr	Val	Leu	Thr	Ile	Leu	Asn	

## Cura 468 SEQ list 0405.txt

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		275					280					285			
Ile	Ala	Ile	Val	Gly	Leu	Ile	Leu	Leu	Glu	Asp	Glu	Gln	Pro	Gly	Leu
	290					295					300				
Val	Ile	Ser	His	His	Ala	Asp	His	Thr	Leu	Ser	Ser	Phe	Cys	Gln	Trp
305					310					315					320
Gln	Ser	Gly	Leu	Met	Gly	Lys	Asp	Gly	Thr	Arg	His	Asp	His	Ala	Ile
				325					330					335	
Leu	Leu	Thr	Gly	Leu	Asp	Ile	Cys	Ser	Trp	Lys	Asn	Glu	Pro	Cys	Asp
			340					345					350		
Thr	Leu	Gly	Phe	Ala	Pro	Ile	Ser	Gly	Met	Cys	Ser	Lys	Tyr	Arg	Ser
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Cys	Thr	Ile	Asn	Glu	Asp	Thr	Gly	Leu	Gly	Leu	Ala	Phe	Thr	Ile	Ala
	370					375					380				
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385					390					395					400
Met	Cys	Lys	Lys	Ser	Glu	Gly	Asn	Ile	Met	Ser	Pro	Thr	Leu	Ala	Gly
				405					410					415	
Arg	Asn	Gly	Val	Phe	Ser	Trp	Ser	Pro	Cys	Ser	Arg	Gln	Tyr	Leu	His
			420					425					430		
Lys	Phe	Leu	Ser	Thr	Ala	Gln	Ala	Ile	Cys	Leu	Ala	Asp	Gln	Pro	Lys
		435					440					445			
Pro	Val	Lys	Glu	Tyr	Lys	Tyr	Pro	Glu	Lys	Leu	Pro	Gly	Glu	Leu	Tyr
	450					455					460				
Gly	Ala	Asn	Thr	Gln	Cys	Lys	Trp	Gln	Phe	Gly	Glu	Lys	Ala	Lys	Leu
465					470					475					480
Cys	Met	Leu	Asp	Phe	Lys	Lys	Asp	Ile	Cys	Lys	Ala	Leu	Trp	Cys	His
				485					490					495	
Arg	Ile	Gly	Arg	Lys	Cys	Glu	Thr	Lys	Phe	Met	Pro	Ala	Ala	Glu	Gly
			500					505					510		
Thr	Ile	Cys	Gly	His	Glu	His	Gly	Ala	Gly	Gly	Gln	Cys	Val	Lys	Tyr

## Cura 468 SEQ list 0405.txt

515					520					525					
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	530					535					540				
Ser	Trp	Ser	Pro	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	His	Arg
545					550					555					560
Ser	Arg	Ser	Gln	Asn	Thr	His	Ser	Arg	Pro	Ser	His	Gly	Gly	Lys	Phe
				565					570					575	
Cys	Glu	Gly	Ser	Thr	Arg	Thr	Leu	Lys	Leu	Cys	Asn	Ser	Gln	Lys	Cys
			580					585					590		
Pro	Arg	Asp	Ser	Val	Asp	Phe	Arg	Ala	Ala	Gln	Cys	Ala	Glu	His	Asn
		595					600					605			
Ser	Arg	Arg	Phe	Arg	Gly	Arg	His	Tyr	Lys	Trp	Lys	Pro	Asp	Gln	Asp
		610				615					620				
Leu	Cys	Lys	Leu	Tyr	Cys	Ile	Ala	Glu	Gly	Phe	Asp	Phe	Phe	Phe	Ser
625					630					635					640
Leu	Ser	Asn	Lys	Val	Lys	Asp	Gly	Thr	Pro	Cys	Ser	Glu	Asp	Ser	Arg
				645					650					655	
Asn	Val	Cys	Ile	Asp	Gly	Ile	Cys	Glu	Arg	Val	Gly	Cys	Asp	Asn	Val
			660					665					670		
Leu	Gly	Ser	Asp	Ala	Val	Glu	Asp	Val	Cys	Gly	Val	Cys	Asn	Gly	Asn
		675					680					685			
Asn	Ser	Ala	Cys	Thr	Ile	His	Arg	Gly	Leu	Tyr	Leu	Glu	Tyr	Tyr	His
		690				695					700				
Met	Val	Thr	Ile	Pro	Ser	Gly	Ala	Arg	Ser	Ile	Arg	Ile	Tyr	Glu	Met
705					710					715					720
Asn	Val	Ser	Thr	Ser	Tyr	Ile	Ser	Val	Arg	Asn	Ala	Leu	Arg	Arg	Tyr
				725					730					735	
Tyr	Leu	Asn	Gly	His	Trp	Thr	Val	Asp	Trp	Pro	Gly	Arg	Tyr	Lys	Phe
			740					745					750		
Ser	Gly	Thr	Thr	Phe	Asp	Tyr	Arg	Arg	Ser	Tyr	Asn	Glu	Pro	Glu	Asn
		755					760					765			
Leu	Ile	Ala	Thr	Gly	Pro	Thr	Asn	Glu	Thr	Leu	Ile	Val	Glu	Leu	Leu

## Cura 468 SEQ list 0405.txt

770

775

780

Phe Gln Gly Arg Asn Pro Gly Val Ala Trp Glu Tyr Ser Met Pro Arg  
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Leu Gly Thr Glu Lys Gln Pro Pro Ala Gln Pro Ser Tyr Thr Trp Ala  
805 810 815

Ile Val Arg Ser Glu Cys Ser Val Ser Cys Gly Gly Gly Arg Cys Leu  
820 825 830

Pro Val Leu Leu Leu Glu Ala Ala Cys Gln Pro Leu Ala Thr Ala Tyr  
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Ile Ala Leu Ala Phe Leu Glu Ser  
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&lt;210&gt; 7

&lt;211&gt; 2895

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 7

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Cura 468 SEQ list 0405.txt

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Cura 468 SEQ list 0405.txt

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 <212> PRT  
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 Arg Gly Asn Arg Gly Ser Gly Gln Leu Glu Ala Ser Pro Pro Arg Leu  
 35 40 45  
 Leu Ser Arg Gly Pro Arg Arg Leu Thr Ala Met Ser Pro Leu Phe Ser  
 50 55 60  
 Ala Gly Thr Cys Val Arg His Gly Thr Arg Ser Gly Ser Ala Trp Glu  
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Cura 468 SEQ list 0405.txt

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		115					120					125				
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His	Met	Asp	Leu	Arg	Thr	Ser	Ser	Ser	Leu	Val	Ala	Pro	Gly	Phe	Ile	
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		195					200					205				
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Tyr	Lys	Trp	Lys	Pro	Tyr	Thr	Gln	Val	Glu	Ala	Asp	Leu	Cys	Lys	Leu	
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	290					295					300					
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Cura 468 SEQ list 0405.txt

Gln	Pro	Pro	Lys	Glu	Asp	Leu	Phe	Ile	Leu	Pro	Asp	Glu	Tyr	Lys	Ser	
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Cura 468 SEQ list 0405.txt

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Cura 468 SEQ list 0405.txt

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Ile	Val	Arg	Ser	Glu	Cys	Ser	Val	Ser	Cys	Gly	Gly	Gly	Arg	Cys	Leu
		915					920					925			
Pro	Val	Leu	Leu	Leu	Glu	Ala	Ala	Cys	Gln	Pro	Ser	Ala	Thr	Ala	Tyr
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<211> 4488

<212> DNA

<213> Homo sapiens

<400> 9

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Cura 468 SEQ list 0405.txt

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Cura 468 SEQ list 0405.txt

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Cura 468 SEQ list 0405.txt

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<212> PRT

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Cura 468 SEQ list 0405.txt

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Cura 468 SEQ list 0405.txt

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Cura 468 SEQ list 0405.txt

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Ser	Thr	Pro	Leu	His	Gln	Ala	Glu	Asp	Ser	Gln	Val	Arg	Gln	Tyr	Phe 735
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Glu	Ala	Val	His	Val	Thr	Val	Pro	Asp	Ala	Ile	Thr	Glu	Trp	Lys	Ala 765
Met	Ser	Phe	Cys	Thr	Ser	Gln	Ser	Arg	Gly	Phe	Gly	Leu	Ser	Pro	Thr 780
Val 785	Gly	Leu	Thr	Ala	Phe	Lys	Pro	Phe	Phe	Val	Asp	Leu	Thr	Leu	Pro 800

Cura 468 SEQ list 0405.txt

Tyr	Ser	Val	Val	Arg	Gly	Glu	Ser	Phe	Arg	Leu	Thr	Ala	Thr	Ile	Phe	
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Asn	Tyr	Leu	Lys	Asp	Cys	Ile	Arg	Val	Gln	Thr	Asp	Leu	Ala	Lys	Ser	
			820					825					830			
His	Glu	Tyr	Gln	Leu	Glu	Ser	Trp	Ala	Asp	Ser	Gln	Thr	Ser	Ser	Cys	
		835					840					845				
Leu	Cys	Ala	Asp	Asp	Ala	Lys	Thr	His	His	Trp	Asn	Ile	Thr	Ala	Val	
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Lys	Leu	Gly	His	Ile	Asn	Phe	Thr	Ile	Ser	Thr	Lys	Ile	Leu	Asp	Ser	
865					870					875					880	
Asn	Glu	Pro	Cys	Gly	Gly	Gln	Lys	Gly	Phe	Val	Pro	Gln	Lys	Gly	Arg	
				885					890					895		
Ser	Asp	Thr	Leu	Ile	Lys	Pro	Val	Leu	Val	Lys	Pro	Glu	Gly	Val	Leu	
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Val	Glu	Lys	Thr	His	Ser	Ser	Leu	Leu	Cys	Pro	Lys	Gly	Gly	Lys	Val	
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Ala	Ser	Glu	Ser	Val	Ser	Leu	Glu	Leu	Pro	Val	Asp	Ile	Val	Pro	Asp	
	930					935					940					
Ser	Thr	Lys	Ala	Tyr	Val	Thr	Val	Leu	Gly	Asp	Ile	Met	Gly	Thr	Ala	
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Leu	Gln	Asn	Leu	Asp	Gly	Leu	Val	Gln	Met	Pro	Ser	Gly	Cys	Gly	Glu	
				965					970					975		
Gln	Asn	Met	Val	Leu	Phe	Ala	Pro	Ile	Ile	Tyr	Val	Leu	Gln	Tyr	Leu	
			980					985					990			
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Phe	Leu	Glu	Ile	Gly	Tyr	Gln	Lys	Glu	Leu	Met	Tyr	Lys	His	Ser	Asn	
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Gly	Ser	Tyr	Ser	Ala	Phe	Gly	Glu	Arg	Asp	Gly	Asn	Gly	Asn	Thr	Trp	
1025				1030					1035					1040		
Leu	Thr	Ala	Phe	Val	Thr	Lys	Cys	Phe	Gly	Gln	Ala	Gln	Lys	Phe	Ile	
			1045					1050					1055			

Cura 468 SEQ list 0405.txt

Phe	Ile	Asp	Pro	Lys	Asn	Ile	Gln	Asp	Ala	Leu	Lys	Trp	Met	Ala	Gly	1060	1065	1070	
Asn	Gln	Leu	Pro	Ser	Gly	Cys	Tyr	Ala	Asn	Val	Gly	Asn	Leu	Leu	His	1075	1080	1085	
Thr	Ala	Met	Lys	Gly	Gly	Val	Asp	Asp	Glu	Val	Ser	Leu	Thr	Ala	Tyr	1090	1095	1100	
Val	Thr	Ala	Ala	Leu	Leu	Glu	Met	Gly	Lys	Asp	Val	Asp	Asp	Pro	Met	1105	1110	1115	1120
Val	Ser	Gln	Gly	Leu	Arg	Cys	Leu	Lys	Asn	Ser	Ala	Thr	Ser	Thr	Thr	1125	1130	1135	
Asn	Leu	Tyr	Thr	Gln	Ala	Leu	Leu	Ala	Tyr	Ile	Phe	Ser	Leu	Ala	Gly	1140	1145	1150	
Glu	Met	Asp	Ile	Arg	Asn	Ile	Leu	Leu	Lys	Gln	Leu	Asp	Gln	Gln	Ala	1155	1160	1165	
Ile	Ile	Ser	Gly	Glu	Ser	Ile	Tyr	Trp	Ser	Gln	Lys	Pro	Thr	Pro	Ser	1170	1175	1180	
Ser	Asn	Ala	Ser	Pro	Trp	Ser	Glu	Pro	Ala	Ala	Val	Asp	Val	Glu	Leu	1185	1190	1195	1200
Thr	Ala	Tyr	Ala	Leu	Leu	Ala	Gln	Leu	Thr	Lys	Pro	Ser	Leu	Thr	Gln	1205	1210	1215	
Lys	Glu	Ile	Ala	Lys	Ala	Thr	Ser	Ile	Val	Ala	Trp	Leu	Ala	Lys	Gln	1220	1225	1230	
His	Asn	Ala	Tyr	Gly	Gly	Phe	Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	1235	1240	1245	
Leu	Gln	Ala	Leu	Ala	Lys	Tyr	Ala	Thr	Thr	Ala	Tyr	Met	Pro	Ser	Glu	1250	1255	1260	
Glu	Ile	Asn	Leu	Val	Val	Lys	Ser	Thr	Glu	Asn	Phe	Gln	Arg	Thr	Phe	1265	1270	1275	1280
Asn	Ile	Gln	Ser	Val	Asn	Arg	Leu	Val	Phe	Gln	Gln	Asp	Thr	Leu	Pro	1285	1290	1295	
Asn	Val	Pro	Gly	Met	Tyr	Thr	Leu	Glu	Ala	Ser	Gly	Gln	Gly	Cys	Val	1300	1305	1310	

Cura 468 SEQ list 0405.txt

Tyr Val Gln Thr Val Leu Arg Tyr Asn Ile Leu Pro Pro Thr Asn Met  
1315 1320 1325

Lys Thr Phe Ser Leu Ser Val Glu Ile Gly Lys Ala Arg Cys Glu Gln  
1330 1335 1340

Pro Thr Ser Pro Arg Ser Leu Thr Leu Thr Ile His Thr Ser Tyr Val  
1345 1350 1355 1360

Gly Ser Arg Ser Ser Ser Asn Met Ala Ile Val Glu Val Lys Met Leu  
1365 1370 1375

Ser Gly Phe Ser Pro Met Glu Gly Thr Asn Gln Leu Leu Leu Gln Gln  
1380 1385 1390

Pro Leu Val Lys Lys Val Glu Phe Gly Thr Asp Thr Leu Asn Ile Tyr  
1395 1400 1405

Leu Asp Glu Leu Ile Lys Asn Thr Gln Thr Tyr Thr Phe Thr Ile Ser  
1410 1415 1420

Gln Ser Val Leu Val Thr Asn Leu Lys Pro Ala Thr Ile Lys Val Tyr  
1425 1430 1435 1440

Asp Tyr Tyr Leu Pro Gly Ser Phe Lys Leu Ser Gln Tyr Thr Ile Val  
1445 1450 1455

Trp Ser Met Asn Asn Asp Ser Ile Val Asp Ser Val Ala Arg His Pro  
1460 1465 1470

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<212> DNA

<213> Homo sapiens

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Cura 468 SEQ list 0405.txt

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ctcatcatgg gctgctgccg gggggcacca tctctaacat tttcaccttc tgggttgatg 360
gagatatgga tctcaggtgc cctgggaatg atgccactct gcatttatct ctacacctgg 420
tcctggagtc ttcagcagaa tctcaccatt ccttatcaga acataggtct gtcttttagga 480
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caccagtctt ggcaaaggac cttgcctatc tttttagggt tagctttcaa gacaccctgt 780
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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Leu Gly Cys Ser Val Glu Ile Arg Lys Leu Trp Ser His Ile Arg Arg



## Cura 468 SEQ list 0405.txt

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Phe	Thr	Ala	Tyr	Leu	Leu	Ala	Ile	Ser	Phe	Ser	Leu	Lys	Pro	Val	Gln	
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Ala	Ile	Ala	Val	Leu	Ile	Met	Gly	Cys	Cys	Arg	Gly	Ala	Pro	Ser	Leu	
			100					105					110			
Thr	Phe	Ser	Pro	Ser	Gly	Leu	Met	Glu	Ile	Trp	Ile	Ser	Gly	Ala	Leu	
		115					120					125				
Gly	Met	Met	Pro	Leu	Cys	Ile	Tyr	Leu	Tyr	Thr	Trp	Ser	Trp	Ser	Leu	
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Gln	Gln	Asn	Leu	Thr	Ile	Pro	Tyr	Gln	Asn	Ile	Gly	Leu	Ser	Leu	Gly	
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Asn	Tyr	Arg	Trp	Pro	Lys	Gln	Ser	Lys	Ile	Ile	Leu	Lys	Ala	Val	Val	
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His	Gln	Ser	Trp	Gln	Arg	Thr	Leu	Pro	Ile	Phe	Leu	Gly	Leu	Ala	Phe	
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		275					280					285				
Leu	Ile	Asp	Gly	Phe	Leu	Ile	Val	Glu	Glu	Arg	Thr	Glu	Asp	Thr	Asp	
	290					295					300					
Cys	Asp	Gly	Ser	Pro	Leu	Pro	Glu	Tyr	Phe	Thr	Glu	Val	Thr	Ile	Ile	

305

310

315

320

Pro Lys Gln Pro Arg Ile  
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&lt;211&gt; 850

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 13

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 ttgaccgatt ccgtggagtg caggacattg tggtaggcaa agggactcac tgtctcatcc 180  
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&lt;211&gt; 272

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

Cura 468 SEQ list 0405.txt

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Gly	His	Arg	Ala	Val	Val	Phe	Asp	Arg	Phe	Arg	Gly	Val	Gln	Asp	Ile
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Val	Val	Gly	Lys	Gly	Thr	His	Cys	Leu	Ile	Pro	Trp	Leu	Gln	Lys	Ser
	50					55					60				
Ile	Ile	Phe	Asp	Cys	Arg	Ser	Gln	Pro	Arg	Asn	Val	Pro	Val	Ile	Thr
65					70					75					80
Gly	Ser	Lys	Asp	Leu	Gln	Asn	Val	Asn	Leu	Thr	Leu	Arg	Ile	Ile	Phe
				85					90					95	
Arg	Pro	Val	Ala	Ser	Gln	Leu	Pro	His	Ile	Phe	Thr	Ser	Ser	Gly	Glu
			100					105					110		
Asp	His	Asp	Glu	Arg	Val	Pro	Pro	Ser	Ile	Thr	Asn	Lys	Ile	Leu	Lys
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Ser	Val	Val	Ala	Arg	Phe	Glu	Ala	Gly	Glu	Leu	Ile	Thr	Gln	Arg	Glu
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Phe	Gly	Leu	Ile	Leu	Asp	Asp	Val	Ser	Leu	Thr	Tyr	Leu	Thr	Phe	Gly
				165					170					175	
Lys	Glu	Phe	Ile	Glu	Ala	Val	Glu	Ala	Lys	Gln	Ile	Ala	Gln	Gln	Glu
			180					185					190		
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Ala	Ala	Ile	Ile	Ser	Ala	Glu	Gly	Asp	Ser	Lys	Val	Ala	Glu	Leu	Ile
	210					215					220				
Thr	Asn	Ser	Leu	Ala	Thr	Ala	Gly	Asp	Ala	Leu	Ile	Glu	Leu	Arg	Lys
225					230					235					240
Leu	Glu	Ala	Val	Glu	Asp	Ile	Thr	Tyr	Gln	Leu	Leu	Arg	Ser	Arg	Asn

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<211> 2011

<212> DNA

<213> Homo sapiens

<400> 15

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Cura 468 SEQ list 0405.txt

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<210> 16  
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Cura 468 SEQ list 0405.txt

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Arg	Cys	Asp	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met
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			180					185					190		
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser
		195					200					205			
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	210					215					220				
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			260					265					270		
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly
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Cura 468 SEQ list 0405.txt

Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys	
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305					310					315					320	
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	
				325					330					335		
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala	
			340					345					350			
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln	
		355					360					365				
Thr	Ala	Thr	Thr	Ala	Gln	Gly	Ser	Ser	Thr	Ala	Ala	Arg	Ser	Ala	Arg	
	370					375					380					
Pro	Ala	Arg	Val	Ser	Ser	Ala	Ser	Ala	Gly	Pro	Leu	Arg	Arg	Arg	Thr	
385					390					395					400	
Ser	Arg	Ser	Ser	Arg	Leu	Pro	Pro	Asn	Arg	Met	His	Asn	Trp	Arg	Arg	
				405					410					415		
Thr	Ser	Ala	Gly	Thr	Gln	Met	Gly	Ile	Ala	Met	Gly	Pro	Gly	Ala	Thr	
			420					425					430			
Arg	Trp	Thr	Gln	Gly	Pro	His	Ser	Thr	Thr	Val	Pro	Cys	Asp	Ala	Ala	
		435					440					445				
Leu	Met	Thr	Ser	Arg	His	Gln	Ser	Trp	Thr	Pro	Gln	Thr	Arg	Cys	Ser	
	450					455					460					
Leu	Arg	Ser	Val	Ala	Arg	Gly	Trp	Ile	Gly	Trp	Ile	Ser	Gly	Val	Pro	
465					470					475					480	
Ser	Cys	Ala	Trp	Leu	Gly	Ala	Ile	Arg	Ala	Thr	His	Pro	Gly	Gln	Ser	
				485					490					495		
Ala	Cys	Gly	Ile	Gly	Met	Leu	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	
			500					505					510			
Gly	Thr	Leu	Phe	Gln	Asn	Pro	Gln	His	Gly	Glu	Pro	Ser	Leu	Gln	Arg	
		515					520					525				
Val	Pro	Val	Ala	Lys	Met	Val	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	
	530					535					540					

Cura 468 SEQ list 0405.txt

Leu	Leu	Lys	Leu	Glu	Arg	Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu
545					550					555					560
Ile	Cys	Leu	Pro	Pro	Glu	Trp	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys
				565					570					575	
Glu	Ile	Ala	Gly	Trp	Gly	Glu	Thr	Lys	Gly	Thr	Gly	Asn	Asp	Thr	Val
			580					585					590		
Leu	Asn	Val	Ala	Leu	Leu	Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Ile
		595					600					605			
Lys	His	Arg	Gly	Arg	Gly	Asp	Tyr	Gly	Gly	Pro	Leu	Ala	Cys	Phe	Thr
	610					615					620				
His	Asn	Cys	Trp	Val	Leu	Glu	Gly	Ile	Ile	Ile	Pro	Asn	Arg	Val	Cys
625					630					635					640
Ala	Arg	Ser	Cys	Trp	Pro	Ala	Val	Phe	Thr	Arg	Val	Ser	Val	Phe	Val
				645					650					655	
Asp	Trp	Ile	His	Lys	Val	Met	Arg	Leu	Gly						
			660					665							

<210> 17  
 <211> 634  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
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 tacatgaagg agggaggagt gggaactgct ttgcgaaaaa tggacgcaat ggccaagcca 180  
 gattgtatca tcacttgtga tggcaaaaac ctcaccataa aaaccgagag cactttgaaa 240  
 acacagtttt cttgtaccct gggagagaag tttgaagaaa ccacagctga tggcagaaaa 300  
 actcagactg tgtgcagctt tgcagatggg gcattgggttc agcatcagga gtgggatggg 360  
 aaggaaaaca caataacaag aaaactgaaa gatgggaaat tagtggtgta ctgtgtcatg 420  
 aacaatgtcg cctgtactcg gatctatgaa aaagtagaat aaaaattcca tcatcacttt 480



Cura 468 SEQ list 0405.txt

ggacaggagt taactaatag aatgatcaag ctcagttcaa tgagcaaadc tccatagtg 540  
 tttttttcat tactgtgttc aattatcttt atcacaaacg tttcacatgc agctatttca 600  
 aagtgtcttg gattaattag gatcatccct ttgg 634

<210> 18  
 <211> 134  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
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 1 5 10 15  
 Lys Arg Phe Asp Glu Tyr Met Lys Glu Gly Gly Val Gly Thr Ala Leu  
 20 25 30  
 Arg Lys Met Asp Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp  
 35 40 45  
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Gln Phe  
 50 55 60  
 Ser Cys Thr Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly Arg  
 65 70 75 80  
 Lys Thr Gln Thr Val Cys Ser Phe Ala Asp Gly Ala Leu Val Gln His  
 85 90 95  
 Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Thr Arg Lys Leu Lys Asp  
 100 105 110  
 Gly Lys Leu Val Val Tyr Cys Val Met Asn Asn Val Ala Cys Thr Arg  
 115 120 125  
 Ile Tyr Glu Lys Val Glu  
 130

<210> 19  
 <211> 822  
 <212> DNA  
 <213> Homo sapiens

<400> 19

Cura 468 SEQ list 0405.txt

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gagccgcatac tggctgtctg tgggtgttcat ctttcgtgtg ctggtgtacg tgggtggcagc 120
ggaggaggtg tgggacgatg agcagaagga ctttgtctgc aacaccaagc agcccggctg 180
ccccaacgtc tgctatgacg agttcttccc cgtgtcccac gtgcgcctct gggccctaca 240
gctcactctg gtcacgtgcc cctcactgct cgtgggtcatg cacgtggcct accgcgagga 300
acgcgagcgc aagcaccacc tgaaacacgg gcccaatgcc ccgtccctgt acgacaacct 360
gagcaagaag cggggcggac tgtgggtggac gtacttgctg agcctcatct tcaaggccgc 420
cgtgggatgct ggcttcctct atatcttcca ccgcctctac aaggattatg acatgccccg 480
cgtgggtggcc tgctccgtgg agccttgccc ccacactgtg gactgttaca tctcccggcc 540
cacggagaag aaggtcttca cctacttcat ggtgaccaca gctgccatct gcatactgct 600
caacctcagt gaagtcttct acctgggtggg caagaggtgc atggagatct tcggccccag 660
gcaccggcgg cctcggtgcc gggaatgcct acccgatacg tgcccacat atgtcctctc 720
ccagggaggg caccctgagg atgggaactc tgtcctaata aaggctgggt cggccccagt 780
ggatgcaggt gggatatccat aacctgagag atcagcagat aa 822

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<210> 20  
 <211> 266  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
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 20 25 30  
 Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln  
 35 40 45  
 Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys  
 50 55 60

Cura 468 SEQ list 0405.txt

Tyr	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln
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Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala
				85					90					95	
Tyr	Arg	Glu	Glu	Arg	Glu	Arg	Lys	His	His	Leu	Lys	His	Gly	Pro	Asn
			100					105					110		
Ala	Pro	Ser	Leu	Tyr	Asp	Asn	Leu	Ser	Lys	Lys	Arg	Gly	Gly	Leu	Trp
		115					120					125			
Trp	Thr	Tyr	Leu	Leu	Ser	Leu	Ile	Phe	Lys	Ala	Ala	Val	Asp	Ala	Gly
	130					135					140				
Phe	Leu	Tyr	Ile	Phe	His	Arg	Leu	Tyr	Lys	Asp	Tyr	Asp	Met	Pro	Arg
145					150					155					160
Val	Val	Ala	Cys	Ser	Val	Glu	Pro	Cys	Pro	His	Thr	Val	Asp	Cys	Tyr
				165					170					175	
Ile	Ser	Arg	Pro	Thr	Glu	Lys	Lys	Val	Phe	Thr	Tyr	Phe	Met	Val	Thr
			180					185					190		
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Ser	Glu	Val	Phe	Tyr	Leu
		195					200					205			
Val	Gly	Lys	Arg	Cys	Met	Glu	Ile	Phe	Gly	Pro	Arg	His	Arg	Arg	Pro
	210					215					220				
Arg	Cys	Arg	Glu	Cys	Leu	Pro	Asp	Thr	Cys	Pro	Pro	Tyr	Val	Leu	Ser
225					230					235					240
Gln	Gly	Gly	His	Pro	Glu	Asp	Gly	Asn	Ser	Val	Leu	Met	Lys	Ala	Gly
				245					250					255	
Ser	Ala	Pro	Val	Asp	Ala	Gly	Gly	Tyr	Pro						
			260					265							

<210> 21

<211> 546

<212> DNA

<213> Homo sapiens

<400> 21

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Cura 468 SEQ list 0405.txt

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 tgtgaactaa atccacagcc acataataat caaacacagaa aagcaaaaga aagccacttc 180  
 aggaaatacc acggtcacac ctcagttggc ttcattgctac agattataga aaatatgttg 240  
 ctgcccgggc caccaatctg ttggttcaca ttactacgtg agcaatgtaa gtgtttgcaa 300  
 gaagccatcc actatctaaa tatcagatat agatgctcca aagcagctac gtcagtgatg 360  
 agaacagaga aaatacgtag caacatttca ttaagttgaa ttctaatact taaaaggctc 420  
 ctttttagtac tgacattctg gatttttaaaa gttatgttga ccgcatgttc tcactcacia 480  
 gtgggagttg aacaatgaga acacacggac acggggaagg gaacatcaca caccagggcc 540  
 tgtcag 546

<210> 22  
 <211> 61  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
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 1 5 10 15  
 Trp Phe Thr Leu Leu Arg Glu Gln Cys Lys Cys Leu Gln Glu Ala Ile  
 20 25 30  
 His Tyr Leu Asn Ile Arg Tyr Arg Cys Ser Lys Ala Ala Thr Ser Val  
 35 40 45  
 Met Arg Thr Glu Lys Ile Arg Ser Asn Ile Ser Leu Ser  
 50 55 60

<210> 23  
 <211> 2309  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (2196)  
 <223> Wherein n is an a o t o r c o r g.

Cura 468 SEQ list 0405.txt

<400> 23

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acaagcatac acaatgggga attgacttct tggaaagata tgccaaattt gttaaagaga 180
ggatagaaat tgaacagAAC tatgcgaaac aattgagaaa tctgggttaag aagtactgcc 240
ccaaacgttc atccaaagat gaagagccac ggtttacctc gtgtgtagcc ttttttaata 300
tccttaatga gttaaatagac tatgcaggac agcgagaagt tgtagcagaa gaaatggcgc 360
acagagtgta tgggtgaatta atgagatatg ctcatactc gaaaactgaa agaaaaatgc 420
atctgcaaga aggacgaaaa gctcaacaat atcttgacat gtgctggaaa cagatgggta 480
atagtaaaaa gaagtttgaa agagaatgta gagaggcaga aaaggcacia cagagttatg 540
aaagattgga taatgatact aatgcaacca aggcagatgt tgaaaatgcc aaacagcagt 600
tgaatctgcg tacgcatatg gccgatgaaa ataaaaatgc atatgctgca caattacaaa 660
actttaatgg agaacaacat aaacatTTTT atgtagtgat tcctcagatt tacaagcaac 720
tacaagaaat ggacgaacga aggactatta aactcagtga gtgttacaga ggatttgctg 780
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ttgaacctcc aggagacttt ccatttgaag attacagtca acatatatat agaaccattt 960
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aagatttcag tcatctgcca ccagaacaga gacgtaaaaa actacagcag cgcattgatg 1140
aacttaacag agaactacag aaagaatcag accaaaaaga tgcactcaac aaaatgaaag 1200
atgtatatga gaaggatcca caaatggggg atccaggagg tttgcagcct aaattagcag 1260
agaccatgaa taacattgac cgcctacgaa tggaaatcca taagaatgag gcttggctct 1320
ctgaagtcga aggcaaaaca ggtgggagag gagacagaag acatagcagt gacataaatc 1380

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Cura 468 SEQ list 0405.txt

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atgatgatcc cttgcctgct attggacact gcaaagctat ctaccctttt gatggacata 1560  
atgaaggtag tctagcaatg aaagaagggtg aagttctcta cattatagag gaggacaaag 1620  
gtgacggatg gacaagagct cggagacaga acggtgaaga aggctacgtt cccacgtcat 1680  
acatagatgt aactctagag aaaaacagta aaggttcctg aagagggttt ctgaggaaat 1740  
gggcaagatg ttgaaggagg ttacatgcag ctgcttttgg gggagggtat tagagttgtc 1800  
aggctcaaag agagtgagag aagcaagttg catgagtga tgcagacatg attttttttt 1860  
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ttttatttta ttgctgtcta atcaataaag aatgcagagc tgtcaaaaaa tgtgtcttac 2040  
atttagctgt cccaacagga ttgtcttccc tcccagctct ggttttaatt ggcttttaga 2100  
cccactatct gtcagatcct tgccatctgt cagtgtctgc ctgcgccacc tccgtgcttg 2160  
cctaacatcc tgttgcatgt ctagcgtgat tgagcnagat tttcaggcat gtcttttagaa 2220  
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<210> 24

<211> 547

<212> PRT

<213> Homo sapiens

<400> 24

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His	Thr	Gln	Trp	Gly	Ile	Asp	Phe	Leu	Glu	Arg	Tyr	Ala	Lys	Phe	Val
				20				25					30		

Lys	Glu	Arg	Ile	Glu	Ile	Glu	Gln	Asn	Tyr	Ala	Lys	Gln	Leu	Arg	Asn
		35					40					45			

Cura 468 SEQ list 0405.txt

Leu	Val	Lys	Lys	Tyr	Cys	Pro	Lys	Arg	Ser	Ser	Lys	Asp	Glu	Glu	Pro
	50					55					60				
Arg	Phe	Thr	Ser	Cys	Val	Ala	Phe	Phe	Asn	Ile	Leu	Asn	Glu	Leu	Asn
65					70				75						80
Asp	Tyr	Ala	Gly	Gln	Arg	Glu	Val	Val	Ala	Glu	Glu	Met	Ala	His	Arg
				85					90					95	
Val	Tyr	Gly	Glu	Leu	Met	Arg	Tyr	Ala	His	Asp	Leu	Lys	Thr	Glu	Arg
			100					105					110		
Lys	Met	His	Leu	Gln	Glu	Gly	Arg	Lys	Ala	Gln	Gln	Tyr	Leu	Asp	Met
		115					120					125			
Cys	Trp	Lys	Gln	Met	Gly	Asn	Ser	Lys	Lys	Lys	Phe	Glu	Arg	Glu	Cys
	130					135					140				
Arg	Glu	Ala	Glu	Lys	Ala	Gln	Gln	Ser	Tyr	Glu	Arg	Leu	Asp	Asn	Asp
145					150					155					160
Thr	Asn	Ala	Thr	Lys	Ala	Asp	Val	Glu	Asn	Ala	Lys	Gln	Gln	Leu	Asn
				165					170					175	
Leu	Arg	Thr	His	Met	Ala	Asp	Glu	Asn	Lys	Asn	Ala	Tyr	Ala	Ala	Gln
			180					185					190		
Leu	Gln	Asn	Phe	Asn	Gly	Glu	Gln	His	Lys	His	Phe	Tyr	Val	Val	Ile
		195					200					205			
Pro	Gln	Ile	Tyr	Lys	Gln	Leu	Gln	Glu	Met	Asp	Glu	Arg	Arg	Thr	Ile
	210					215					220				
Lys	Leu	Ser	Glu	Cys	Tyr	Arg	Gly	Phe	Ala	Asp	Ser	Glu	Arg	Lys	Val
225					230					235					240
Ile	Pro	Ile	Ile	Ser	Lys	Cys	Leu	Glu	Gly	Met	Ile	Leu	Ala	Ala	Lys
				245					250					255	
Ser	Val	Asp	Glu	Arg	Arg	Asp	Ser	Gln	Met	Val	Val	Asp	Ser	Phe	Lys
			260					265					270		
Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Phe	Pro	Phe	Glu	Asp	Tyr	Ser	Gln
		275					280					285			
His	Ile	Tyr	Arg	Thr	Ile	Ser	Asp	Gly	Thr	Ile	Ser	Ala	Ser	Lys	Gln
	290					295					300				

Cura 468 SEQ list 0405.txt

Glu	Ser	Gly	Lys	Met	Asp	Ala	Lys	Thr	Pro	Val	Gly	Lys	Ala	Lys	Gly	305	310	315									320
Lys	Leu	Trp	Leu	Phe	Gly	Lys	Lys	Pro	Lys	Gly	Pro	Ala	Leu	Glu	Asp		325	330								335	
Phe	Ser	His	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Arg		340	345								350	
Ile	Asp	Glu	Leu	Asn	Arg	Glu	Leu	Gln	Lys	Glu	Ser	Asp	Gln	Lys	Asp		355	360								365	
Ala	Leu	Asn	Lys	Met	Lys	Asp	Val	Tyr	Glu	Lys	Asp	Pro	Gln	Met	Gly		370	375									
Asp	Pro	Gly	Ser	Leu	Gln	Pro	Lys	Leu	Ala	Glu	Thr	Met	Asn	Asn	Ile	385		390								400	
Asp	Arg	Leu	Arg	Met	Glu	Ile	His	Lys	Asn	Glu	Ala	Trp	Leu	Ser	Glu		405	410								415	
Val	Glu	Gly	Lys	Thr	Gly	Gly	Arg	Gly	Asp	Arg	Arg	His	Ser	Ser	Asp		420	425								430	
Ile	Asn	His	Leu	Val	Thr	Gln	Gly	Arg	Glu	Ser	Pro	Glu	Gly	Ser	Tyr		435	440								445	
Thr	Asp	Asp	Ala	Asn	Gln	Glu	Val	Arg	Gly	Pro	Pro	Gln	Gln	His	Gly	450		455								460	
His	His	Asn	Glu	Phe	Asp	Asp	Glu	Phe	Glu	Asp	Asp	Asp	Pro	Leu	Pro	465		470								480	
Ala	Ile	Gly	His	Cys	Lys	Ala	Ile	Tyr	Pro	Phe	Asp	Gly	His	Asn	Glu		485	490								495	
Gly	Thr	Leu	Ala	Met	Lys	Glu	Gly	Glu	Val	Leu	Tyr	Ile	Ile	Glu	Glu		500	505								510	
Asp	Lys	Gly	Asp	Gly	Trp	Thr	Arg	Ala	Arg	Arg	Gln	Asn	Gly	Glu	Glu		515	520								525	
Gly	Tyr	Val	Pro	Thr	Ser	Tyr	Ile	Asp	Val	Thr	Leu	Glu	Lys	Asn	Ser	530		535								540	
Lys	Gly	Ser														545											



Cura 468 SEQ list 0405.txt

<210> 25  
 <211> 1787  
 <212> DNA  
 <213> Homo sapiens

<400> 25

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ggatcttcag agcagagcct ggagaccagc agcatcccat ttctcaggcg gtgtgctggc 180
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acctcactga catcaaactc aacagttccc aggagtttgc tcagctctct cctagactgg 600
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Cura 468 SEQ list 0405.txt

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catggcgctt agtgggggtg gtcagctggg ggcgtggctg cgcagagccc aatcacccag 1380  
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gatgaactgg gtaagagtat gcctgagttt gtatcccaga tctaccattt cctgtgtcga 1680  
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<210> 26  
<211> 1787  
<212> DNA  
<213> Homo sapiens

<400> 26  
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tggtagatct gggatacaaa ctcaggcata ctcttaccga gttcatcctt aaactgatag 180  
aatccaatg gattccatgt ttaagcttca cttcttcctc cactcactct ggggaatatg 240  
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ctctgcgcag ccacgcccc agctgaccac cccactagg cgccatgtgt ccccatctgg 480  
gcacactagg gggccccgcg tatctccctg gcatgcatca gcccttccgt ccaggtagcc 540  
agcgcaaagc atgcgggggg tgagggtcc gctgtacacg caagagctgt tgcagagctg 600

Cura 468 SEQ list 0405.txt

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agtgctgagc aggggacacca ccgtgtcctg gagcatatcc gagctgtaag tatggctagg 660
gtgggtgtgg cccagaccag acacccagca ccgcgagccc ttcggaaaat gctgttcctt 720
ggccggcagg cacacagcgc ccacagtgtc tgagaagttg agagcgggtct ggagcctcag 780
gagggcgacg tcgtagtcat gattctgggc actgtagagg ggggtgtggga taatcctctc 840
caccagagcc ccttgggtggg gcctgacggc actgtggctg accagccccg catgaacccg 900
ccagctggac aggcggggcca gcctgaaact gtgcatacaa tgtgcagcag tcaccaccca 960
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cgctccacac tcagagcatc tgagggaaac aacttgacca gaagtgcagt tgttcctaac 1140
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gagctgagca aactcctggg aactgttgag tttgatgtca gtgaggttta ctcccttgtg 1260
gtgagtgagt ctgagatgcc caaggctcca gcagatctgc agccccaggg cggggctcca 1320
gccctcatgg cagaccagga gccagcgtgg ctgateccctc acttgcgctt ccagcaagaa 1380
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ctgagaaatg ggatgctgct ggtctccagg ctctgctctg aagatcccag gtcctgggcc 1680
ctcctctgca tactgggcct ccataggggg ttggatcatcc agcatcaggc tcataggggt 1740
cagtggcact gttgtaaagc ctcagggtct actaggcaat gttccgc 1787

```

<210> 27  
 <211> 472  
 <212> PRT  
 <213> Homo sapiens

<400> 27

## Cura 468 SEQ list 0405.txt

Met	Ser	Leu	Met	Leu	Asp	Asp	Gln	Pro	Pro	Met	Glu	Ala	Gln	Tyr	Ala			
1				5					10					15				
Glu	Glu	Gly	Pro	Gly	Pro	Gly	Ile	Phe	Arg	Ala	Glu	Pro	Gly	Asp	Gln			
			20					25					30					
Gln	His	Pro	Ile	Ser	Gln	Ala	Val	Cys	Trp	Arg	Ser	Met	Arg	Arg	Gly			
		35					40					45						
Cys	Ala	Val	Leu	Gly	Ala	Leu	Gly	Leu	Leu	Ala	Gly	Ala	Gly	Val	Gly			
	50					55					60							
Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Cys	Pro	Ala	Ala	Ser	Gln	Pro	Ile			
65					70					75					80			
Ser	Gly	Thr	Leu	Gln	Asp	Glu	Glu	Ile	Thr	Leu	Ser	Cys	Ser	Glu	Ala			
				85					90					95				
Ser	Ala	Glu	Glu	Ala	Leu	Leu	Pro	Ala	Leu	Pro	Lys	Thr	Val	Ser	Phe			
			100					105					110					
Arg	Ile	Asn	Ser	Glu	Asp	Phe	Leu	Leu	Glu	Ala	Gln	Val	Arg	Asp	Gln			
		115					120					125						
Pro	Arg	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly			
	130					135					140							
Leu	Gln	Ile	Cys	Trp	Ser	Leu	Gly	His	Leu	Arg	Leu	Thr	His	His	Lys			
145					150					155					160			
Gly	Val	Asn	Leu	Thr	Asp	Ile	Lys	Leu	Asn	Ser	Ser	Gln	Glu	Phe	Ala			
				165					170					175				
Gln	Leu	Ser	Pro	Arg	Leu	Gly	Gly	Phe	Leu	Glu	Glu	Ala	Trp	Gln	Pro			
			180					185					190					
Ser	Arg	Thr	Thr	Glu	Ala	Val	Arg	Asn	Asn	Cys	Thr	Ser	Gly	Gln	Val			
		195					200					205						
Val	Ser	Leu	Arg	Cys	Ser	Glu	Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg			
	210					215					220							
Ile	Val	Gly	Gly	Gln	Ser	Val	Ala	Pro	Gly	Arg	Trp	Pro	Trp	Gln	Ala			
225					230					235					240			
Ser	Val	Ala	Leu	Gly	Phe	Arg	His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala			
				245					250					255				

Cura 468 SEQ list 0405.txt

Pro	Arg	Trp	Val	Val	Thr	Ala	Ala	His	Cys	Met	His	Ser	Phe	Arg	Leu	260	265	270
Ala	Arg	Leu	Ser	Ser	Trp	Arg	Val	His	Ala	Gly	Leu	Val	Ser	His	Ser	275	280	285
Ala	Val	Arg	Pro	His	Gln	Gly	Ala	Leu	Val	Glu	Arg	Ile	Ile	Pro	His	290	295	300
Pro	Leu	Tyr	Ser	Ala	Gln	Asn	His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Arg	305	310	315
Leu	Gln	Thr	Ala	Leu	Asn	Phe	Ser	Asp	Thr	Val	Gly	Ala	Val	Cys	Leu	325	330	335
Pro	Ala	Lys	Glu	Gln	His	Phe	Pro	Lys	Gly	Ser	Arg	Cys	Trp	Val	Ser	340	345	350
Gly	Trp	Gly	His	Thr	His	Pro	Ser	His	Thr	Tyr	Ser	Ser	Asp	Met	Leu	355	360	365
Gln	Asp	Thr	Val	Val	Pro	Leu	Leu	Ser	Thr	Gln	Leu	Cys	Asn	Ser	Ser	370	375	380
Cys	Val	Tyr	Ser	Gly	Ala	Leu	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	Tyr	385	390	395
Leu	Asp	Gly	Arg	Ala	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	405	410	415
Val	Cys	Pro	Asp	Gly	Asp	Thr	Trp	Arg	Leu	Val	Gly	Val	Val	Ser	Trp	420	425	430
Gly	Arg	Gly	Cys	Ala	Glu	Pro	Asn	His	Pro	Gly	Val	Tyr	Ala	Lys	Val	435	440	445
Ala	Glu	Phe	Leu	Asp	Trp	Ile	His	Asp	Thr	Ala	Gln	Val	Ser	Val	Gly	450	455	460
Ala	Gly	Val	Gly	Gln	Gly	Asp	Phe									465	470	

<210> 28

<211> 2148

<212> DNA

<213> Homo sapiens

## Cura 468 SEQ list 0405.txt

&lt;400&gt; 28

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gaccctgagg ctttacaaca gtgctactga cccctatgag cctgatgctg gatgaccaac 180
cccctatgga ggcccagtat gcagaggagg gcccaggacc tgggatcttc agagcagagc 240
ctggagacca gcagcatccc atttctcagg cgggtgtgctg gcgttccatg cgacgtggct 300
gtgcagtgct gggagccctg gggctgctgg ccggtgcagg tggttggtca tggctcctag 360
tgctgtatct gtgtcctgct gcctctcagc ccatttccgg gaccttgcag gatgaggaga 420
taactttgag ctgctcagag gccagcgctg aggaagctct gctccctgca ctccccaaaa 480
cagtatcttt cagaataaac agcgaagact tcttgctgga agcgcaagtg agggatcagc 540
cacgctggct cctgggtctgc catgagggct ggagccccgc cctggggctg cagatctgct 600
ggagccttgg gcatctcaga ctcactcacc acaagggagt aaacctcact gacatcaaac 660
tcaacagttc ccaggagttt gctcagctct ctccctagact gggaggcttc ctggaggagg 720
cgtggcagcc caggaacaac tgcacttctg gtcaagttgt tccctcaga tgctctgagt 780
gtggagcgag gccctggct tcccggatag ttggtgggca gtctgtggct cctgggcgct 840
ggccgtggca ggccagcgtg gccctgggct tccggcacac gtgtgggggc tctgtgctag 900
cgccacgctg ggtgggtgact gctgcacatt gtatgcacag tgcccagaat catgactacg 960
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gcctgccggc caaggaacag cattttccga agggctcgcg gtgctgggtg tccggctgggt 1080
gccacacca ccctagccat acttacagct cggatatgct ccaggacacg gtgggtgcccc 1140
tgctcagcac tcagctctgc aacagctctt gcgtgtacag cggagccctc accccccgca 1200
tgctttgcgc tggctacctg gacggaaggg ctgatgcatg ccagggagat agcggggggcc 1260
ccctagtgtg ccagatggg gacacatggc gcctagtggg ggtggtcagc tgggggctg 1320
gctgcgcaga gcccaatcac ccaggtgtct acgccaaggt agctgagttt ctggactgga 1380
tccatgacac tgctcaggac tccctcctct gagtcctgct gtttcctcca gtctcactgc 1440

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Cura 468 SEQ list 0405.txt

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actggccagc caccagcca acaggtctct cctcttgggc cctgatttca gagtcctctt 1620
tctcactaga gactcaatga cagaagagag gctgggactt ggttgggcat gctgtggttg 1680
ctgaggggatg agggggagga gagaggtagg agctggagat gaagagactg ctagaagcag 1740
caggaagcct gcccttctgc cctctcccct ccctgccct gtgtgagtct tttagggagg 1800
gtgactggga ggtgcccccc gtcccacctt tttcctgtgc tctaggtggg ctaagtgcct 1860
ccctagagga ctccatggct gagaggctcc tgggcagatg gggccaaggc tgggccagtc 1920
ccagatgaag cctatgggag tcaggaccct ctccactctc cctctccact ccccttcctg 1980
ttctcacctg gctgtggctg gccctgtgtg ggggtgggtac actggaaaac aagaagggtg 2040
gagttgggtct aggacattgg ttttaaataga cagttctgtg aactgggtcca aggaggttct 2100
gttattaaag tgatatatgg tcttgaaaaa aaaaaaaaaa aaaaaaaaaa 2148

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<210> 29  
 <211> 418  
 <212> PRT  
 <213> Homo sapiens

<400> 29  
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 Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln  
 20 25 30  
 Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly  
 35 40 45  
 Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly  
 50 55 60  
 Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile  
 65 70 75 80

## Cura 468 SEQ list 0405.txt

Ser	Gly	Thr	Leu	Gln	Asp	Glu	Glu	Ile	Thr	Leu	Ser	Cys	Ser	Glu	Ala
				85					90					95	
Ser	Ala	Glu	Glu	Ala	Leu	Leu	Pro	Ala	Leu	Pro	Lys	Thr	Val	Ser	Phe
			100					105					110		
Arg	Ile	Asn	Ser	Glu	Asp	Phe	Leu	Leu	Glu	Ala	Gln	Val	Arg	Asp	Gln
		115					120					125			
Pro	Arg	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly
	130					135					140				
Leu	Gln	Ile	Cys	Trp	Ser	Leu	Gly	His	Leu	Arg	Leu	Thr	His	His	Lys
145					150					155					160
Gly	Val	Asn	Leu	Thr	Asp	Ile	Lys	Leu	Asn	Ser	Ser	Gln	Glu	Phe	Ala
				165					170					175	
Gln	Leu	Ser	Pro	Arg	Leu	Gly	Gly	Phe	Leu	Glu	Glu	Ala	Trp	Gln	Pro
			180					185					190		
Arg	Asn	Asn	Cys	Thr	Ser	Gly	Gln	Val	Val	Ser	Leu	Arg	Cys	Ser	Glu
		195					200					205			
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ser	Val
	210					215					220				
Ala	Pro	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Ala	Leu	Gly	Phe	Arg
225					230					235					240
His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala	Pro	Arg	Trp	Val	Val	Thr	Ala
				245					250					255	
Ala	His	Cys	Met	His	Ser	Ala	Gln	Asn	His	Asp	Tyr	Asp	Val	Ala	Leu
			260					265					270		
Leu	Arg	Leu	Gln	Thr	Ala	Leu	Asn	Phe	Ser	Asp	Thr	Val	Gly	Ala	Val
		275					280					285			
Cys	Leu	Pro	Ala	Lys	Glu	Gln	His	Phe	Pro	Lys	Gly	Ser	Arg	Cys	Trp
	290					295					300				
Val	Ser	Gly	Trp	Cys	His	Thr	His	Pro	Ser	His	Thr	Tyr	Ser	Ser	Asp
305					310					315					320
Met	Leu	Gln	Asp	Thr	Val	Val	Pro	Leu	Leu	Ser	Thr	Gln	Leu	Cys	Asn
				325					330					335	



Cura 468 SEQ list 0405.txt

Ser Ser Cys Val Tyr Ser Gly Ala Leu Thr Pro Arg Met Leu Cys Ala  
340 345 350

Gly Tyr Leu Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly  
355 360 365

Pro Leu Val Cys Pro Asp Gly Asp Thr Trp Arg Leu Val Gly Val Val  
370 375 380

Ser Trp Gly Arg Gly Cys Ala Glu Pro Asn His Pro Gly Val Tyr Ala  
385 390 395 400

Lys Val Ala Glu Phe Leu Asp Trp Ile His Asp Thr Ala Gln Asp Ser  
405 410 415

Leu Leu

<210> 30  
<211> 1593  
<212> PRT  
<213> Homo sapiens

<400> 30  
Met Pro Cys Ala Gln Arg Ser Trp Leu Ala Asn Leu Ser Val Val Ala  
1 5 10 15

Gln Leu Leu Asn Phe Gly Ala Leu Cys Tyr Gly Arg Gln Pro Gln Pro  
20 25 30

Gly Pro Val Arg Phe Pro Asp Arg Arg Gln Glu His Phe Ile Lys Gly  
35 40 45

Leu Pro Glu Tyr His Val Val Gly Pro Val Arg Val Asp Ala Ser Gly  
50 55 60

His Phe Leu Ser Tyr Gly Leu His Tyr Pro Ile Thr Ser Ser Arg Arg  
65 70 75 80

Lys Arg Asp Leu Asp Gly Ser Glu Asp Trp Val Tyr Tyr Arg Ile Ser  
85 90 95

His Glu Glu Lys Asp Leu Phe Phe Asn Leu Thr Val Asn Gln Gly Phe  
100 105 110

Leu Ser Asn Ser Tyr Ile Met Glu Lys Arg Tyr Gly Asn Leu Ser His  
115 120 125

Cura 468 SEQ list 0405.txt

Val	Lys	Met	Met	Ala	Ser	Ser	Ala	Pro	Leu	Cys	His	Leu	Ser	Gly	Thr	
	130					135					140					
Val	Leu	Gln	Gln	Gly	Thr	Arg	Val	Gly	Thr	Ala	Ala	Leu	Ser	Ala	Cys	
145					150					155					160	
His	Gly	Leu	Thr	Gly	Phe	Phe	Gln	Leu	Pro	His	Gly	Asp	Phe	Phe	Ile	
				165					170					175		
Glu	Pro	Val	Lys	Lys	His	Pro	Leu	Val	Glu	Gly	Gly	Tyr	His	Pro	His	
			180					185					190			
Ile	Val	Tyr	Arg	Arg	Gln	Lys	Val	Pro	Glu	Thr	Lys	Glu	Pro	Thr	Cys	
		195					200					205				
Gly	Leu	Lys	Asp	Ser	Val	Asn	Ile	Ser	Gln	Lys	Gln	Glu	Leu	Trp	Arg	
	210					215					220					
Glu	Lys	Trp	Glu	Arg	His	Asn	Leu	Pro	Ser	Arg	Ser	Leu	Ser	Arg	Arg	
225					230					235					240	
Ser	Ile	Ser	Lys	Glu	Arg	Trp	Val	Glu	Thr	Leu	Val	Val	Ala	Asp	Thr	
				245					250					255		
Lys	Met	Ile	Glu	Tyr	His	Gly	Ser	Glu	Asn	Val	Glu	Ser	Tyr	Ile	Leu	
			260					265					270			
Thr	Ile	Met	Asn	Met	Val	Thr	Gly	Leu	Phe	His	Asn	Pro	Ser	Ile	Gly	
		275					280					285				
Asn	Ala	Ile	His	Ile	Val	Val	Val	Arg	Leu	Ile	Leu	Leu	Glu	Glu	Glu	
	290					295					300					
Glu	Gln	Gly	Leu	Lys	Ile	Val	His	His	Ala	Glu	Lys	Thr	Leu	Ser	Ser	
305					310					315					320	
Phe	Cys	Lys	Trp	Gln	Lys	Ser	Ile	Asn	Pro	Lys	Ser	Asp	Leu	Asn	Pro	
				325					330					335		
Val	His	His	Asp	Val	Ala	Val	Leu	Leu	Thr	Arg	Lys	Asp	Ile	Cys	Ala	
			340					345					350			
Gly	Phe	Asn	Arg	Pro	Cys	Glu	Thr	Leu	Gly	Leu	Ser	His	Leu	Ser	Gly	
		355					360					365				
Met	Cys	Gln	Pro	His	Arg	Ser	Cys	Asn	Ile	Asn	Glu	Asp	Ser	Gly	Leu	
	370					375					380					

Cura 468 SEQ list 0405.txt

Pro	Leu	Ala	Phe	Thr	Ile	Ala	His	Glu	Leu	Gly	His	Ser	Phe	Gly	Ile	385	390	395				400
Gln	His	Asp	Gly	Lys	Glu	Asn	Asp	Cys	Glu	Pro	Val	Gly	Arg	His	Pro		405	410				415
Tyr	Ile	Met	Ser	Arg	Gln	Leu	Gln	Tyr	Asp	Pro	Thr	Pro	Leu	Thr	Trp		420	425				430
Ser	Lys	Cys	Ser	Glu	Glu	Tyr	Ile	Thr	Arg	Phe	Leu	Asp	Arg	Gly	Trp		435	440				445
Gly	Phe	Cys	Leu	Asp	Asp	Ile	Pro	Lys	Lys	Lys	Gly	Leu	Lys	Ser	Lys		450	455				460
Val	Ile	Ala	Pro	Gly	Val	Ile	Tyr	Asp	Val	His	His	Gln	Cys	Gln	Leu	465	470	475				480
Gln	Tyr	Gly	Pro	Asn	Ala	Thr	Phe	Cys	Gln	Glu	Val	Glu	Asn	Val	Cys		485	490				495
Gln	Thr	Leu	Trp	Cys	Ser	Val	Lys	Gly	Phe	Cys	Arg	Ser	Lys	Leu	Asp		500	505				510
Ala	Ala	Ala	Asp	Gly	Thr	Gln	Cys	Gly	Glu	Lys	Lys	Trp	Cys	Met	Ala		515	520				525
Gly	Lys	Cys	Ile	Thr	Val	Gly	Lys	Lys	Pro	Glu	Ser	Ile	Pro	Gly	Gly		530	535				540
Trp	Gly	Arg	Trp	Ser	Pro	Trp	Ser	His	Cys	Ser	Arg	Thr	Cys	Gly	Ala	545	550	555				560
Gly	Val	Gln	Ser	Ala	Glu	Arg	Leu	Cys	Asn	Asn	Pro	Glu	Pro	Lys	Phe		565	570				575
Gly	Gly	Lys	Tyr	Cys	Thr	Gly	Glu	Arg	Lys	Arg	Tyr	Arg	Leu	Cys	Asn		580	585				590
Val	His	Pro	Cys	Arg	Ser	Glu	Ala	Pro	Thr	Phe	Arg	Gln	Met	Gln	Cys		595	600				605
Ser	Glu	Phe	Asp	Thr	Val	Pro	Tyr	Lys	Asn	Glu	Leu	Tyr	His	Trp	Phe		610	615				620
Pro	Ile	Phe	Asn	Pro	Ala	His	Pro	Cys	Glu	Leu	Tyr	Cys	Arg	Pro	Ile	625	630	635				640

Cura 468 SEQ list 0405.txt

Asp	Gly	Gln	Phe	Ser 645	Glu	Lys	Met	Leu	Asp 650	Ala	Val	Ile	Asp	Gly 655	Thr	
Pro	Cys	Phe	Glu	Gly	Gly	Asn	Ser	Arg 665	Asn	Val	Cys	Ile	Asn 670	Gly	Ile	
Cys	Lys	Met	Val	Gly	Cys	Asp	Tyr 680	Glu	Ile	Asp	Ser	Asn 685	Ala	Thr	Glu	
Asp 690	Arg	Cys	Gly	Val	Cys	Leu 695	Gly	Asp	Gly	Ser	Ser 700	Cys	Gln	Thr	Val	
Arg 705	Lys	Met	Phe	Lys	Gln 710	Lys	Glu	Gly	Ser	Gly 715	Tyr	Val	Asp	Ile	Gly 720	
Leu	Ile	Pro	Lys	Gly 725	Ala	Arg	Asp	Ile	Arg 730	Val	Met	Glu	Ile	Glu 735	Gly	
Ala	Gly	Asn	Phe	Leu	Ala	Ile	Arg	Ser 745	Glu	Asp	Pro	Glu	Lys 750	Tyr	Tyr	
Leu	Asn 755	Gly	Gly	Phe	Ile	Ile	Gln 760	Trp	Asn	Gly	Asn 765	Tyr	Lys	Leu	Ala	
Gly 770	Thr	Val	Phe	Gln	Tyr	Asp 775	Arg	Lys	Gly	Asp	Leu 780	Glu	Lys	Leu	Met	
Ala 785	Thr	Gly	Pro	Thr	Asn 790	Glu	Ser	Val	Trp	Ile 795	Gln	Leu	Leu	Phe	Gln 800	
Val	Thr	Asn	Pro	Gly 805	Ile	Lys	Tyr	Glu	Tyr 810	Thr	Ile	Gln	Lys	Asp 815	Gly	
Leu	Asp	Asn	Asp 820	Val	Glu	Gln	Met	Tyr 825	Phe	Trp	Gln	Tyr	Gly 830	His	Trp	
Thr	Glu	Cys 835	Ser	Val	Thr	Cys	Gly 840	Thr	Gly	Ile	Arg	Arg 845	Gln	Thr	Ala	
His 850	Cys	Ile	Lys	Lys	Gly	Arg 855	Gly	Met	Val	Lys	Ala 860	Thr	Phe	Cys	Asp	
Pro 865	Glu	Thr	Gln	Pro	Asn 870	Gly	Arg	Gln	Lys	Lys 875	Cys	His	Glu	Lys	Ala 880	
Cys	Pro	Pro	Arg	Trp 885	Trp	Ala	Gly	Glu	Trp 890	Glu	Ala	Cys	Ser	Ala 895	Thr	

Cura 468 SEQ list 0405.txt

Cys	Gly	Pro	His	Gly	Glu	Lys	Lys	Arg	Thr	Val	Leu	Cys	Ile	Gln	Thr	
			900					905					910			
Met	Val	Ser	Asp	Glu	Gln	Ala	Leu	Pro	Pro	Thr	Asp	Cys	Gln	His	Leu	
		915					920					925				
Leu	Lys	Pro	Lys	Thr	Leu	Leu	Ser	Cys	Asn	Arg	Asp	Ile	Leu	Cys	Pro	
	930					935					940					
Ser	Asp	Trp	Thr	Val	Gly	Asn	Trp	Ser	Glu	Cys	Ser	Val	Ser	Cys	Gly	
945					950					955					960	
Gly	Gly	Val	Arg	Ile	Arg	Ser	Val	Thr	Cys	Ala	Lys	Asn	His	Asp	Glu	
				965					970					975		
Pro	Cys	Asp	Val	Thr	Arg	Lys	Pro	Asn	Ser	Arg	Ala	Leu	Cys	Gly	Leu	
			980					985					990			
Gln	Gln	Cys	Pro	Ser	Ser	Arg	Arg	Val	Leu	Lys	Pro	Asn	Lys	Gly	Thr	
		995					1000					1005				
Ile	Ser	Asn	Gly	Lys	Asn	Pro	Pro	Thr	Leu	Lys	Pro	Val	Pro	Pro	Pro	
	1010					1015					1020					
Thr	Ser	Arg	Pro	Arg	Met	Leu	Thr	Thr	Pro	Thr	Gly	Pro	Glu	Ser	Met	
1025					1030					1035					1040	
Ser	Thr	Ser	Thr	Pro	Ala	Ile	Ser	Ser	Pro	Ser	Pro	Thr	Thr	Ala	Ser	
				1045					1050					1055		
Lys	Glu	Gly	Asp	Leu	Gly	Gly	Lys	Gln	Trp	Gln	Asp	Ser	Ser	Thr	Gln	
			1060					1065					1070			
Pro	Glu	Leu	Ser	Ser	Arg	Tyr	Leu	Ile	Ser	Thr	Gly	Ser	Thr	Ser	Gln	
		1075					1080					1085				
Pro	Ile	Leu	Thr	Ser	Gln	Ser	Leu	Ser	Ile	Gln	Pro	Ser	Glu	Glu	Asn	
	1090					1095					1100					
Val	Ser	Ser	Ser	Asp	Thr	Gly	Pro	Thr	Ser	Glu	Gly	Gly	Leu	Val	Ala	
1105					1110					1115					1120	
Thr	Thr	Thr	Ser	Gly	Ser	Gly	Leu	Ser	Ser	Ser	Arg	Asn	Pro	Ile	Thr	
				1125					1130					1135		
Trp	Pro	Val	Thr	Pro	Phe	Tyr	Asn	Thr	Leu	Thr	Lys	Gly	Pro	Glu	Met	
			1140					1145					1150			

Cura 468 SEQ list 0405.txt

Glu Ile His Ser Gly Ser Gly Glu Glu Arg Glu Gln Pro Glu Asp Lys	1155	1160	1165
Asp Glu Ser Asn Pro Val Ile Trp Thr Lys Ile Arg Val Pro Gly Asn	1170	1175	1180
Asp Ala Pro Val Glu Ser Thr Glu Met Pro Leu Ala Pro Pro Leu Thr	1185	1190	1195 1200
Pro Asp Leu Ser Arg Glu Ser Trp Trp Pro Pro Phe Ser Thr Val Met	1205	1210	1215
Glu Gly Leu Leu Pro Ser Gln Arg Pro Thr Thr Ser Glu Thr Gly Thr	1220	1225	1230
Pro Arg Val Glu Gly Met Val Thr Glu Lys Pro Ala Asn Thr Leu Leu	1235	1240	1245
Pro Leu Gly Gly Asp His Gln Pro Glu Pro Ser Gly Lys Thr Ala Asn	1250	1255	1260
Arg Asn His Leu Lys Leu Pro Asn Asn Met Asn Gln Thr Lys Ser Ser	1265	1270	1275 1280
Glu Pro Val Leu Thr Glu Glu Asp Ala Thr Ser Leu Ile Thr Glu Gly	1285	1290	1295
Phe Leu Leu Asn Ala Ser Asn Tyr Lys Gln Leu Thr Asn Gly His Gly	1300	1305	1310
Ser Ala His Trp Ile Val Gly Asn Trp Ser Glu Cys Ser Thr Thr Cys	1315	1320	1325
Gly Leu Gly Ala Tyr Trp Lys Arg Val Glu Cys Thr Thr Gln Met Asp	1330	1335	1340
Ser Asp Cys Ala Ala Ile Gln Arg Pro Asp Pro Ala Lys Arg Cys His	1345	1350	1355 1360
Leu Arg Pro Cys Ala Gly Trp Lys Val Gly Asn Trp Ser Lys Cys Ser	1365	1370	1375
Arg Asn Cys Ser Gly Gly Phe Lys Ile Arg Glu Ile Gln Cys Val Asp	1380	1385	1390
Ser Arg Asp His Arg Asn Leu Arg Pro Phe His Cys Gln Phe Leu Ala	1395	1400	1405

Cura 468 SEQ list 0405.txt

Gly Ile Pro Pro Pro Leu Ser Met Ser Cys Asn Pro Glu Pro Cys Glu  
1410 1415 1420

Ala Trp Gln Val Glu Pro Trp Ser Gln Cys Ser Arg Ser Cys Gly Gly  
1425 1430 1435 1440

Gly Val Gln Glu Arg Gly Val Phe Cys Pro Gly Gly Leu Cys Asp Trp  
1445 1450 1455

Thr Lys Arg Pro Thr Ser Thr Met Ser Cys Asn Glu His Leu Cys Cys  
1460 1465 1470

His Trp Ala Thr Gly Asn Trp Asp Leu Cys Ser Thr Ser Cys Gly Gly  
1475 1480 1485

Gly Phe Gln Lys Arg Ile Val Gln Cys Val Pro Ser Glu Gly Asn Lys  
1490 1495 1500

Thr Glu Asp Gln Asp Gln Cys Leu Cys Asp His Lys Pro Arg Pro Pro  
1505 1510 1515 1520

Glu Phe Lys Lys Cys Asn Gln Gln Ala Cys Lys Lys Ser Ala Asp Leu  
1525 1530 1535

Leu Cys Thr Lys Asp Lys Leu Ser Ala Ser Phe Cys Gln Thr Leu Lys  
1540 1545 1550

Ala Met Lys Lys Cys Ser Val Pro Thr Val Arg Ala Glu Cys Cys Phe  
1555 1560 1565

Ser Cys Pro Gln Thr His Ile Thr His Thr Gln Arg Gln Arg Arg Gln  
1570 1575 1580

Arg Leu Leu Gln Lys Ser Lys Glu Leu  
1585 1590

<210> 31

<211> 1077

<212> PRT

<213> Homo sapiens

<400> 31

Arg Ser Gln Asp Glu Phe Leu Ser Ser Leu Glu Ser Tyr Glu Ile Ala  
1 5 10 15

Phe Pro Thr Arg Val Asp His Asn Gly Ala Leu Leu Ala Phe Ser Pro

## Cura 468 SEQ list 0405.txt

20

25

30

Pro	Pro	Pro	Arg	Arg	Gln	Arg	Arg	Gly	Thr	Gly	Ala	Thr	Ala	Glu	Ser
		35					40					45			
Arg	Leu	Phe	Tyr	Lys	Val	Ala	Ser	Pro	Ser	Thr	His	Phe	Leu	Leu	Asn
	50					55					60				
Leu	Thr	Arg	Ser	Ser	Arg	Leu	Leu	Ala	Gly	His	Val	Ser	Val	Glu	Tyr
65					70					75					80
Trp	Thr	Arg	Glu	Gly	Leu	Ala	Trp	Gln	Arg	Ala	Ala	Arg	Pro	His	Cys
				85					90					95	
Leu	Tyr	Ala	Gly	His	Leu	Gln	Gly	Gln	Ala	Ser	Ser	Ser	His	Val	Ala
			100					105					110		
Ile	Ser	Thr	Cys	Gly	Gly	Leu	His	Gly	Leu	Ile	Val	Ala	Asp	Glu	Glu
		115					120					125			
Glu	Tyr	Leu	Ile	Glu	Pro	Leu	His	Gly	Gly	Pro	Lys	Gly	Ser	Arg	Ser
	130					135					140				
Pro	Glu	Glu	Ser	Gly	Pro	His	Val	Val	Tyr	Lys	Arg	Ser	Ser	Leu	Arg
145					150					155					160
His	Pro	His	Leu	Asp	Thr	Ala	Cys	Gly	Val	Arg	Asp	Glu	Lys	Pro	Trp
				165					170					175	
Lys	Gly	Arg	Pro	Trp	Trp	Leu	Arg	Thr	Leu	Lys	Pro	Pro	Pro	Ala	Arg
			180					185					190		
Pro	Leu	Gly	Asn	Glu	Thr	Glu	Arg	Gly	Gln	Pro	Gly	Leu	Lys	Arg	Ser
		195					200					205			
Val	Ser	Arg	Glu	Arg	Tyr	Val	Glu	Thr	Leu	Val	Val	Ala	Asp	Lys	Met
	210					215					220				
Met	Val	Ala	Tyr	His	Gly	Arg	Arg	Asp	Val	Glu	Gln	Tyr	Val	Leu	Ala
225					230					235					240
Ile	Met	Asn	Ile	Val	Ala	Lys	Leu	Phe	Gln	Asp	Ser	Ser	Leu	Gly	Ser
				245					250					255	
Thr	Val	Asn	Ile	Leu	Val	Thr	Arg	Leu	Ile	Leu	Leu	Thr	Glu	Asp	Gln
			260					265					270		
Pro	Thr	Leu	Glu	Ile	Thr	His	His	Ala	Gly	Lys	Ser	Leu	Asp	Ser	Phe



## Cura 468 SEQ list 0405.txt

275					280					285					
Cys	Lys	Trp	Gln	Lys	Ser	Ile	Val	Asn	His	Ser	Gly	His	Gly	Asn	Ala
	290					295					300				
Ile	Pro	Glu	Asn	Gly	Val	Ala	Asn	His	Asp	Thr	Ala	Val	Leu	Ile	Thr
305					310					315					320
Arg	Tyr	Asp	Ile	Cys	Ile	Tyr	Lys	Asn	Lys	Pro	Cys	Gly	Thr	Leu	Gly
				325					330					335	
Leu	Ala	Pro	Val	Gly	Gly	Met	Cys	Glu	Arg	Glu	Arg	Ser	Cys	Ser	Val
			340					345					350		
Asn	Glu	Asp	Ile	Gly	Leu	Pro	Gln	Ala	Phe	Thr	Ile	Ala	His	Glu	Ile
		355					360					365			
Gly	His	Thr	Phe	Gly	Met	Asn	His	Asp	Gly	Val	Gly	Asn	Ser	Cys	Gly
	370					375					380				
Ala	Arg	Gly	Gln	Asp	Pro	Ala	Lys	Leu	Met	Ala	Ala	His	Ile	Thr	Met
385					390					395					400
Lys	Thr	Asn	Pro	Phe	Val	Trp	Ser	Ser	Cys	Asn	Arg	Asp	Tyr	Ile	Thr
				405					410					415	
Ser	Phe	Leu	Asp	Ser	Gly	Leu	Gly	Leu	Cys	Leu	Asn	Asn	Arg	Pro	Pro
			420					425					430		
Arg	Gln	Asp	Phe	Val	Tyr	Pro	Thr	Val	Ala	Pro	Gly	Gln	Ala	Tyr	Asp
		435					440					445			
Ala	Asp	Glu	Gln	Cys	Arg	Phe	Gln	His	Gly	Val	Lys	Ser	Arg	Gln	Cys
	450					455					460				
Lys	Tyr	Gly	Glu	Val	Cys	Ser	Glu	Leu	Trp	Cys	Leu	Ser	Lys	Ser	Asn
465					470					475					480
Arg	Cys	Ile	Thr	Asn	Ser	Ile	Pro	Ala	Ala	Glu	Gly	Thr	Leu	Cys	Gln
				485					490					495	
Thr	His	Thr	Ile	Asp	Lys	Gly	Trp	Cys	Tyr	Lys	Arg	Val	Cys	Val	Pro
			500					505					510		
Phe	Gly	Ser	Arg	Pro	Glu	Gly	Val	Asp	Gly	Ala	Trp	Gly	Pro	Trp	Thr
		515					520					525			
Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	Ser	Ser

## Cura 468 SEQ list 0405.txt

530

535

540

Ser 545	Arg	His	Cys	Asp	Ser 550	Pro	Arg	Pro	Thr	Ile 555	Gly	Gly	Lys	Tyr	Cys 560
Leu	Gly	Glu	Arg	Arg 565	Arg	His	Arg	Ser	Cys 570	Asn	Thr	Asp	Asp	Cys 575	Pro
Pro	Gly	Ser	Gln 580	Asp	Phe	Arg	Glu	Val 585	Gln	Cys	Ser	Glu	Phe 590	Asp	Ser
Ile	Pro	Phe 595	Arg	Gly	Lys	Phe	Tyr 600	Lys	Trp	Lys	Thr	Tyr 605	Arg	Gly	Gly
Gly 610	Val	Lys	Ala	Cys	Ser	Leu 615	Thr	Ser	Leu	Ala	Glu 620	Gly	Phe	Asn	Phe
Tyr 625	Thr	Glu	Arg	Ala	Ala 630	Ala	Val	Val	Asp	Gly 635	Thr	Pro	Cys	Arg	Pro 640
Asp	Thr	Val	Asp	Ile 645	Cys	Val	Ser	Gly	Glu 650	Cys	Lys	His	Val	Gly 655	Cys
Asp	Arg	Val	Leu 660	Gly	Ser	Asp	Leu	Arg 665	Glu	Asp	Lys	Cys	Arg 670	Val	Cys
Gly	Gly	Asp 675	Gly	Ser	Ala	Cys	Glu 680	Thr	Ile	Glu	Gly	Val 685	Phe	Ser	Pro
Ala 690	Ser	Pro	Gly	Ala	Gly	Tyr 695	Glu	Asp	Val	Val	Trp 700	Ile	Pro	Lys	Gly
Ser 705	Val	His	Ile	Phe	Ile 710	Gln	Asp	Leu	Asn	Leu 715	Ser	Leu	Ser	His	Leu 720
Ala	Leu	Lys	Gly	Asp 725	Gln	Glu	Ser	Leu	Leu 730	Leu	Glu	Gly	Leu	Pro 735	Gly
Thr	Pro	Gln	Pro 740	His	Arg	Leu	Pro	Leu	Ala 745	Gly	Thr	Thr	Phe 750	Gln	Leu
Arg	Gln	Gly 755	Pro	Asp	Gln	Val	Gln 760	Ser	Leu	Glu	Ala	Leu 765	Gly	Pro	Ile
Asn 770	Ala	Ser	Leu	Ile	Val	Met 775	Val	Leu	Ala	Arg	Thr 780	Glu	Leu	Pro	Ala
Leu	Arg	Tyr	Arg	Phe	Asn	Ala	Pro	Ile	Ala	Arg	Asp	Ser	Leu	Pro	Pro

## Cura 468 SEQ list 0405.txt

785																
Tyr	Ser	Trp	His	Tyr	Ala	Pro	Trp	Thr	Lys	Cys	Ser	Ala	Gln	Cys	Ala	
				805					810					815		
Gly	Gly	Ser	Gln	Val	Gln	Ala	Val	Glu	Cys	Arg	Asn	Gln	Leu	Asp	Ser	
			820					825					830			
Ser	Ala	Val	Ala	Pro	His	Tyr	Cys	Ser	Ala	His	Ser	Lys	Leu	Pro	Lys	
		835					840					845				
Arg	Gln	Arg	Ala	Cys	Asn	Thr	Glu	Pro	Cys	Pro	Pro	Asp	Trp	Val	Val	
	850					855					860					
Gly	Asn	Trp	Ser	Leu	Cys	Ser	Arg	Ser	Cys	Asp	Ala	Gly	Val	Arg	Ser	
865					870					875					880	
Arg	Ser	Val	Val	Cys	Gln	Arg	Arg	Val	Ser	Ala	Ala	Glu	Glu	Lys	Ala	
				885					890					895		
Leu	Asp	Asp	Ser	Ala	Cys	Pro	Gln	Pro	Arg	Pro	Pro	Val	Leu	Glu	Ala	
			900					905					910			
Cys	His	Gly	Pro	Thr	Cys	Pro	Pro	Glu	Trp	Ala	Ala	Leu	Asp	Trp	Ser	
		915					920					925				
Glu	Cys	Thr	Pro	Ser	Cys	Gly	Pro	Gly	Leu	Arg	His	Arg	Val	Val	Leu	
	930					935					940					
Cys	Lys	Ser	Ala	Asp	His	Arg	Ala	Thr	Leu	Pro	Pro	Ala	His	Cys	Ser	
945					950					955					960	
Pro	Ala	Ala	Lys	Pro	Pro	Ala	Thr	Met	Arg	Cys	Asn	Leu	Arg	Arg	Cys	
				965					970					975		
Pro	Pro	Ala	Arg	Trp	Val	Ala	Gly	Glu	Trp	Gly	Glu	Cys	Ser	Ala	Gln	
			980					985					990			
Cys	Gly	Val	Gly	Gln	Arg	Gln	Arg	Ser	Val	Arg	Cys	Thr	Ser	His	Thr	
		995				1000						1005				
Gly	Gln	Ala	Ser	His	Glu	Cys	Thr	Glu	Ala	Leu	Arg	Pro	Pro	Thr	Thr	
	1010					1015					1020					
Gln	Gln	Cys	Glu	Ala	Lys	Cys	Asp	Ser	Pro	Thr	Pro	Gly	Asp	Gly	Pro	
1025					1030					1035					1040	
Glu	Glu	Cys	Lys	Asp	Val	Asn	Lys	Val	Ala	Tyr	Cys	Pro	Leu	Val	Leu	

1045

1050

1055

Lys Phe Gln Phe Cys Ser Arg Ala Tyr Phe Arg Gln Met Cys Cys Lys  
 1060 1065 1070

Thr Cys Gln Gly His  
 1075

&lt;210&gt; 32

&lt;211&gt; 997

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 32

Met Pro Gly Gly Pro Ser Pro Arg Ser Pro Ala Pro Leu Leu Arg Pro  
 1 5 10 15

Leu Leu Leu Leu Leu Cys Ala Leu Ala Pro Gly Ala Pro Gly Pro Ala  
 20 25 30

Pro Gly Arg Ala Thr Glu Gly Arg Ala Ala Leu Asp Ile Val His Pro  
 35 40 45

Val Arg Val Asp Ala Gly Gly Ser Phe Leu Ser Tyr Glu Leu Trp Pro  
 50 55 60

Arg Ala Leu Arg Lys Arg Asp Val Ser Val Arg Arg Asp Ala Pro Ala  
 65 70 75 80

Phe Tyr Glu Leu Gln Tyr Arg Gly Arg Glu Leu Arg Phe Asn Leu Thr  
 85 90 95

Ala Asn Gln His Leu Leu Ala Pro Gly Phe Val Ser Glu Thr Arg Arg  
 100 105 110

Arg Gly Gly Leu Gly Arg Ala His Ile Arg Ala His Thr Pro Ala Cys  
 115 120 125

His Leu Leu Gly Glu Val Gln Asp Pro Glu Leu Glu Gly Gly Leu Ala  
 130 135 140

Ala Ile Ser Ala Cys Asp Gly Leu Lys Gly Val Phe Gln Leu Ser Asn  
 145 150 155 160

Glu Asp Tyr Phe Ile Glu Pro Leu Asp Ser Ala Pro Ala Arg Pro Gly  
 165 170 175

## Cura 468 SEQ list 0405.txt

His	Ala	Gln	Pro	His	Val	Val	Tyr	Lys	Arg	Gln	Ala	Pro	Glu	Arg	Leu
			180					185					190		
Ala	Gln	Arg	Gly	Asp	Ser	Ser	Ala	Pro	Ser	Thr	Cys	Gly	Val	Gln	Val
		195					200					205			
Tyr	Pro	Glu	Leu	Glu	Ser	Arg	Arg	Glu	Arg	Trp	Glu	Gln	Arg	Gln	Gln
	210					215					220				
Trp	Arg	Arg	Pro	Arg	Leu	Arg	Arg	Leu	His	Gln	Arg	Ser	Val	Ser	Lys
225					230					235					240
Glu	Lys	Trp	Val	Glu	Thr	Leu	Val	Val	Ala	Asp	Ala	Lys	Met	Val	Glu
				245					250					255	
Tyr	His	Gly	Gln	Pro	Gln	Val	Glu	Ser	Tyr	Val	Leu	Thr	Ile	Met	Asn
			260					265					270		
Met	Val	Ala	Gly	Leu	Phe	His	Asp	Pro	Ser	Ile	Gly	Asn	Pro	Ile	His
		275					280					285			
Ile	Thr	Ile	Val	Arg	Leu	Val	Leu	Leu	Glu	Asp	Glu	Glu	Glu	Asp	Leu
	290					295					300				
Lys	Ile	Thr	His	His	Ala	Asp	Asn	Thr	Leu	Lys	Ser	Phe	Cys	Lys	Trp
305					310					315					320
Gln	Lys	Ser	Ile	Asn	Met	Lys	Gly	Asp	Ala	His	Pro	Leu	His	His	Asp
				325					330					335	
Thr	Ala	Ile	Leu	Leu	Thr	Arg	Lys	Asp	Leu	Cys	Ala	Ala	Met	Asn	Arg
			340					345					350		
Pro	Cys	Glu	Thr	Leu	Gly	Leu	Ser	His	Val	Ala	Gly	Met	Cys	Gln	Pro
		355					360					365			
His	Arg	Ser	Cys	Ser	Ile	Asn	Glu	Asp	Thr	Gly	Leu	Pro	Leu	Ala	Phe
	370					375					380				
Thr	Val	Ala	His	Glu	Leu	Gly	His	Ser	Phe	Gly	Ile	Gln	His	Asp	Gly
385					390					395					400
Ser	Gly	Asn	Asp	Cys	Glu	Pro	Val	Gly	Lys	Arg	Pro	Phe	Ile	Met	Ser
				405					410					415	
Pro	Gln	Leu	Leu	Tyr	Asp	Ala	Ala	Pro	Leu	Thr	Trp	Ser	Arg	Cys	Ser
			420					425					430		

Cura 468 SEQ list 0405.txt

Arg	Gln	Tyr	Ile	Thr	Arg	Phe	Leu	Asp	Arg	Gly	Trp	Gly	Leu	Cys	Leu
		435					440					445			
Asp	Asp	Pro	Pro	Ala	Lys	Asp	Ile	Ile	Asp	Phe	Pro	Ser	Val	Pro	Pro
	450					455					460				
Gly	Val	Leu	Tyr	Asp	Val	Ser	His	Gln	Cys	Arg	Leu	Gln	Tyr	Gly	Ala
465					470					475					480
Tyr	Ser	Ala	Phe	Cys	Glu	Asp	Met	Asp	Asn	Val	Cys	His	Thr	Leu	Trp
				485					490					495	
Cys	Ser	Val	Gly	Thr	Thr	Cys	His	Ser	Lys	Leu	Asp	Ala	Ala	Val	Asp
			500					505					510		
Gly	Thr	Arg	Cys	Gly	Glu	Asn	Lys	Trp	Cys	Leu	Ser	Gly	Glu	Cys	Val
		515					520					525			
Pro	Val	Gly	Phe	Arg	Pro	Glu	Ala	Val	Asp	Gly	Gly	Trp	Ser	Gly	Trp
	530					535					540				
Ser	Ala	Trp	Ser	Ile	Cys	Ser	Arg	Ser	Cys	Gly	Met	Gly	Val	Gln	Ser
545					550					555					560
Ala	Glu	Arg	Gln	Cys	Thr	Gln	Pro	Thr	Pro	Lys	Tyr	Lys	Gly	Arg	Tyr
				565					570					575	
Cys	Val	Gly	Glu	Arg	Lys	Arg	Phe	Arg	Leu	Cys	Asn	Leu	Gln	Ala	Cys
			580					585					590		
Pro	Ala	Gly	Arg	Pro	Ser	Phe	Arg	His	Val	Gln	Cys	Ser	His	Phe	Asp
		595					600					605			
Ala	Met	Leu	Tyr	Lys	Gly	Gln	Leu	His	Thr	Trp	Val	Pro	Val	Val	Asn
	610					615					620				
Asp	Val	Asn	Pro	Cys	Glu	Leu	His	Cys	Arg	Pro	Ala	Asn	Glu	Tyr	Phe
625					630					635					640
Ala	Lys	Lys	Leu	Arg	Asp	Ala	Val	Val	Asp	Gly	Thr	Pro	Cys	Tyr	Gln
				645					650					655	
Val	Arg	Ala	Ser	Arg	Asp	Leu	Cys	Ile	Asn	Gly	Ile	Cys	Lys	Asn	Val
			660					665					670		
Gly	Cys	Asp	Phe	Glu	Ile	Asp	Ser	Gly	Ala	Met	Glu	Asp	Arg	Cys	Gly
		675					680					685			

## Cura 468 SEQ list 0405.txt

Val	Cys	His	Gly	Asn	Gly	Ser	Thr	Cys	His	Thr	Val	Ser	Gly	Thr	Phe
690						695					700				
Glu	Glu	Ala	Glu	Gly	Leu	Gly	Tyr	Val	Asp	Val	Gly	Leu	Ile	Pro	Ala
705					710					715					720
Gly	Ala	Arg	Glu	Ile	Arg	Ile	Gln	Glu	Val	Ala	Glu	Ala	Ala	Asn	Phe
				725					730					735	
Leu	Ala	Leu	Arg	Ser	Glu	Asp	Pro	Glu	Lys	Tyr	Phe	Leu	Asn	Gly	Gly
			740					745					750		
Trp	Thr	Ile	Gln	Trp	Asn	Gly	Asp	Tyr	Gln	Val	Ala	Gly	Thr	Thr	Phe
		755					760					765			
Thr	Tyr	Ala	Arg	Arg	Gly	Asn	Trp	Glu	Asn	Leu	Thr	Ser	Pro	Gly	Pro
	770					775					780				
Thr	Lys	Glu	Pro	Val	Trp	Ile	Gln	Val	Pro	Ala	Ser	Arg	Gly	Pro	Gly
785					790					795					800
Gly	Gly	Ser	Arg	Gly	Gly	Val	Pro	Arg	Pro	Ser	Thr	Leu	His	Gly	Arg
				805					810					815	
Ser	Arg	Pro	Gly	Gly	Val	Ser	Pro	Gly	Ser	Val	Thr	Glu	Pro	Gly	Ser
			820					825					830		
Glu	Pro	Gly	Pro	Pro	Ala	Ala	Ala	Ser	Thr	Ser	Val	Ser	Pro	Ser	Leu
		835					840					845			
Lys	Trp	Pro	Asn	Leu	Val	Ala	Ala	Val	His	Arg	Gly	Gly	Trp	Gly	Gln
	850					855					860				
Ala	Pro	Leu	Gly	Leu	Gly	Gly	Trp	Arg	Arg	His	Leu	Val	Leu	Met	Gly
865					870					875					880
Pro	Arg	Leu	Pro	Thr	Gln	Leu	Leu	Phe	Gln	Glu	Ser	Asn	Pro	Gly	Val
				885					890					895	
His	Tyr	Glu	Tyr	Thr	Ile	His	Arg	Glu	Ala	Gly	Gly	His	Asp	Glu	Val
			900					905					910		
Pro	Pro	Pro	Val	Phe	Ser	Trp	His	Tyr	Gly	Pro	Trp	Thr	Lys	Cys	Thr
		915					920					925			
Val	Thr	Cys	Gly	Arg	Gly	Glu	Lys	Trp	Gly	Arg	His	Ser	Pro	Thr	Cys
	930					935					940				

Cura 468 SEQ list 0405.txt

Arg Gly Leu Val Ser Gly Gln Gly His Trp Leu Gln Leu Pro Ala His  
945 950 955 960

Cys Trp Ala Thr Thr Gly Leu Glu Val Cys Phe Ser Glu Pro Gln Phe  
965 970 975

Ser Ile Cys Glu Met Arg Leu Ala Ile Ala Leu Cys Pro Arg Pro Ala  
980 985 990

Gly Arg Val His Gly  
995

<210> 33

<211> 854

<212> PRT

<213> Homo sapiens

<400> 33

Met Met Val Ala Tyr His Gly Arg Arg Asp Val Glu Gln Tyr Val Leu  
1 5 10 15

Ala Ile Met Asn Ile Val Ala Lys Leu Phe Gln Asp Ser Ser Leu Gly  
20 25 30

Ser Thr Val Asn Ile Leu Val Thr Arg Leu Ile Leu Leu Thr Glu Asp  
35 40 45

Gln Pro Thr Leu Glu Ile Thr His His Ala Gly Lys Ser Leu Asp Ser  
50 55 60

Phe Cys Lys Trp Gln Lys Ser Ile Val Asn His Ser Gly His Gly Asn  
65 70 75 80

Ala Ile Pro Glu Asn Gly Val Ala Asn His Asp Thr Ala Val Leu Ile  
85 90 95

Thr Arg Tyr Asp Ile Cys Ile Tyr Lys Asn Lys Pro Cys Gly Thr Leu  
100 105 110

Gly Leu Ala Pro Val Gly Gly Met Cys Glu Arg Glu Arg Ser Cys Ser  
115 120 125

Val Asn Glu Asp Ile Gly Leu Ala Thr Ala Phe Thr Ile Ala His Glu  
130 135 140

Ile Gly His Thr Phe Gly Met Asn His Asp Gly Val Gly Asn Ser Cys  
145 150 155 160



Cura 468 SEQ list 0405.txt

Gly	Ala	Arg	Gly	Gln	Asp	Pro	Ala	Lys	Leu	Met	Ala	Ala	His	Ile	Thr	165	170	175
Met	Lys	Thr	Asn	Pro	Phe	Val	Trp	Ser	Ser	Cys	Ser	Arg	Asp	Tyr	Ile	180	185	190
Thr	Ser	Phe	Leu	Asp	Ser	Gly	Leu	Gly	Leu	Cys	Leu	Asn	Asn	Arg	Pro	195	200	205
Pro	Arg	Gln	Asp	Phe	Val	Tyr	Pro	Thr	Val	Ala	Pro	Gly	Gln	Ala	Tyr	210	215	220
Asp	Ala	Asp	Glu	Gln	Cys	Arg	Phe	Gln	His	Gly	Val	Lys	Ser	Arg	Gln	225	230	235
Cys	Lys	Tyr	Gly	Glu	Val	Cys	Ser	Glu	Leu	Trp	Cys	Leu	Ser	Lys	Ser	245	250	255
Asn	Arg	Cys	Ile	Thr	Asn	Ser	Ile	Pro	Ala	Ala	Glu	Gly	Thr	Leu	Cys	260	265	270
Gln	Thr	His	Thr	Ile	Asp	Lys	Gly	Trp	Cys	Tyr	Lys	Arg	Val	Cys	Val	275	280	285
Pro	Phe	Gly	Ser	Arg	Pro	Glu	Gly	Val	Asp	Gly	Ala	Trp	Gly	Pro	Trp	290	295	300
Thr	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	Ser	Ser	305	310	315
Ser	Ser	Arg	His	Cys	Asp	Ser	Pro	Arg	Pro	Thr	Ile	Gly	Gly	Lys	Tyr	325	330	335
Cys	Leu	Gly	Glu	Arg	Arg	Arg	His	Arg	Ser	Cys	Asn	Thr	Asp	Asp	Cys	340	345	350
Pro	Pro	Gly	Ser	Gln	Asp	Phe	Arg	Glu	Val	Gln	Cys	Ser	Glu	Phe	Asp	355	360	365
Ser	Ile	Pro	Phe	Arg	Gly	Lys	Phe	Tyr	Lys	Trp	Lys	Thr	Tyr	Arg	Gly	370	375	380
Gly	Gly	Val	Lys	Ala	Cys	Ser	Leu	Thr	Cys	Leu	Ala	Glu	Gly	Phe	Asn	385	390	395
Phe	Tyr	Thr	Glu	Arg	Ala	Ala	Ala	Val	Val	Asp	Gly	Thr	Pro	Cys	Arg	405	410	415

Cura 468 SEQ list 0405.txt

Pro	Asp	Thr	Val	Asp	Ile	Cys	Val	Ser	Gly	Glu	Cys	Lys	His	Val	Gly	420	425	430
Cys	Asp	Arg	Val	Leu	Gly	Ser	Asp	Leu	Arg	Glu	Asp	Lys	Cys	Arg	Val	435	440	445
Cys	Gly	Gly	Asp	Gly	Ser	Ala	Cys	Glu	Thr	Ile	Glu	Gly	Val	Phe	Ser	450	455	460
Pro	Ala	Ser	Pro	Gly	Ala	Gly	Tyr	Glu	Asp	Val	Val	Trp	Ile	Pro	Lys	465	470	475
Gly	Ser	Val	His	Ile	Phe	Ile	Gln	Asp	Leu	Asn	Leu	Ser	Leu	Ser	His	485	490	495
Leu	Ala	Leu	Lys	Gly	Asp	Gln	Glu	Ser	Leu	Leu	Leu	Glu	Gly	Leu	Pro	500	505	510
Gly	Thr	Pro	Gln	Pro	His	Arg	Leu	Pro	Leu	Ala	Gly	Thr	Thr	Phe	Gln	515	520	525
Leu	Arg	Gln	Gly	Pro	Asp	Gln	Val	Gln	Ser	Leu	Glu	Ala	Leu	Gly	Pro	530	535	540
Ile	Asn	Ala	Ser	Leu	Ile	Val	Met	Val	Leu	Ala	Arg	Thr	Glu	Leu	Pro	545	550	555
Ala	Leu	Arg	Tyr	Arg	Phe	Asn	Ala	Pro	Ile	Ala	Arg	Asp	Ser	Leu	Pro	565	570	575
Pro	Tyr	Ser	Trp	His	Tyr	Ala	Pro	Trp	Thr	Lys	Cys	Ser	Ala	Gln	Cys	580	585	590
Ala	Gly	Gly	Ser	Gln	Val	Gln	Ala	Val	Glu	Cys	Arg	Asn	Gln	Leu	Asp	595	600	605
Ser	Ser	Ala	Val	Ala	Pro	His	Tyr	Cys	Ser	Ala	His	Ser	Lys	Leu	Pro	610	615	620
Lys	Arg	Gln	Arg	Ala	Cys	Asn	Thr	Glu	Pro	Cys	Pro	Pro	Asp	Trp	Val	625	630	635
Val	Gly	Asn	Trp	Ser	Leu	Cys	Ser	Arg	Ser	Cys	Asp	Ala	Gly	Val	Arg	645	650	655
Ser	Arg	Ser	Val	Val	Cys	Gln	Arg	Arg	Val	Ser	Ala	Ala	Glu	Glu	Lys	660	665	670

Cura 468 SEQ list 0405.txt

Ala	Leu	Asp	Asp	Ser	Ala	Cys	Pro	Gln	Pro	Arg	Pro	Pro	Val	Leu	Glu	
		675					680					685				
Ala	Cys	His	Gly	Pro	Thr	Cys	Pro	Pro	Glu	Trp	Ala	Ala	Leu	Asp	Trp	
	690					695					700					
Ser	Glu	Cys	Thr	Pro	Ser	Cys	Gly	Pro	Gly	Leu	Arg	His	Arg	Val	Val	
705					710					715					720	
Leu	Cys	Lys	Ser	Ala	Asp	His	Arg	Ala	Thr	Leu	Pro	Pro	Ala	His	Cys	
				725					730					735		
Ser	Pro	Ala	Ala	Lys	Pro	Pro	Ala	Thr	Met	Arg	Cys	Asn	Leu	Arg	Arg	
			740					745					750			
Cys	Pro	Pro	Ala	Arg	Trp	Val	Ala	Gly	Glu	Trp	Gly	Glu	Cys	Ser	Ala	
		755					760					765				
Gln	Cys	Gly	Val	Gly	Gln	Arg	Gln	Arg	Ser	Val	Arg	Cys	Thr	Ser	His	
	770					775					780					
Thr	Gly	Gln	Ala	Ser	His	Glu	Cys	Thr	Glu	Ala	Leu	Arg	Pro	Pro	Thr	
785					790					795					800	
Thr	Gln	Gln	Cys	Glu	Ala	Lys	Cys	Asp	Ser	Pro	Thr	Pro	Gly	Asp	Gly	
				805					810					815		
Pro	Glu	Glu	Cys	Lys	Asp	Val	Asn	Lys	Val	Ala	Tyr	Cys	Pro	Leu	Val	
			820					825					830			
Leu	Lys	Phe	Gln	Phe	Cys	Ser	Arg	Ala	Tyr	Phe	Arg	Gln	Met	Cys	Cys	
		835					840					845				
Lys	Thr	Cys	His	Gly	His											
	850															

<210> 34  
 <211> 860  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <221> VARIANT  
 <222> (450)  
 <223> Wherein Xaa is any amino acid.

## Cura 468 SEQ list 0405.txt

&lt;400&gt; 34

Met	Glu	Ile	Leu	Trp	Lys	Thr	Leu	Thr	Trp	Ile	Leu	Ser	Leu	Ile	Met
1				5					10					15	
Ala	Ser	Ser	Glu	Phe	His	Ser	Asp	His	Arg	Leu	Ser	Tyr	Ser	Ser	Gln
			20					25					30		
Glu	Glu	Phe	Leu	Thr	Tyr	Leu	Glu	His	Tyr	Gln	Leu	Thr	Ile	Pro	Ile
		35					40					45			
Arg	Val	Asp	Gln	Asn	Gly	Ala	Phe	Leu	Ser	Phe	Thr	Val	Lys	Asn	Asp
	50					55					60				
Lys	His	Ser	Arg	Arg	Arg	Arg	Ser	Met	Asp	Pro	Ile	Asp	Pro	Gln	Gln
65					70					75					80
Ala	Val	Ser	Lys	Leu	Phe	Phe	Lys	Leu	Ser	Ala	Tyr	Gly	Lys	His	Phe
				85					90					95	
His	Leu	Asn	Leu	Thr	Leu	Asn	Thr	Asp	Phe	Val	Ser	Lys	His	Phe	Thr
			100					105					110		
Val	Glu	Tyr	Trp	Gly	Lys	Asp	Gly	Pro	Gln	Trp	Lys	His	Asp	Phe	Leu
		115					120					125			
Asp	Asn	Cys	His	Tyr	Thr	Gly	Tyr	Leu	Gln	Asp	Gln	Arg	Ser	Thr	Thr
	130					135					140				
Lys	Val	Ala	Leu	Ser	Asn	Cys	Val	Gly	Leu	His	Gly	Val	Ile	Ala	Thr
145					150					155					160
Glu	Asp	Glu	Glu	Tyr	Phe	Ile	Glu	Pro	Leu	Lys	Asn	Thr	Thr	Glu	Asp
				165					170					175	
Ser	Lys	His	Phe	Ser	Tyr	Glu	Asn	Gly	His	Pro	His	Val	Ile	Tyr	Lys
			180					185					190		
Lys	Ser	Ala	Leu	Gln	Gln	Arg	His	Leu	Tyr	Asp	His	Ser	His	Cys	Gly
		195					200					205			
Val	Ser	Asp	Phe	Thr	Arg	Ser	Gly	Lys	Pro	Trp	Trp	Leu	Asn	Asp	Thr
	210					215					220				
Ser	Thr	Val	Ser	Tyr	Ser	Leu	Pro	Ile	Asn	Asn	Thr	His	Ile	His	His
225					230					235					240
Arg	Gln	Lys	Arg	Ser	Val	Ser	Ile	Glu	Arg	Phe	Val	Glu	Thr	Leu	Val
				245					250					255	

Cura 468 SEQ list 0405.txt

Val	Ala	Asp	Lys	Met	Met	Val	Gly	Tyr	His	Gly	Arg	Lys	Asp	Ile	Glu	260	265	270
His	Tyr	Ile	Leu	Ser	Val	Met	Asn	Ile	Val	Ala	Lys	Leu	Tyr	Arg	Asp	275	280	285
Ser	Ser	Leu	Gly	Asn	Val	Val	Asn	Ile	Ile	Val	Ala	Arg	Leu	Ile	Val	290	295	300
Leu	Thr	Glu	Asp	Gln	Pro	Asn	Leu	Glu	Ile	Asn	His	His	Ala	Asp	Lys	305	310	315
Ser	Leu	Asp	Ser	Phe	Cys	Lys	Trp	Gln	Lys	Ser	Ile	Leu	Ser	His	Gln	325	330	335
Ser	Asp	Gly	Asn	Thr	Ile	Pro	Glu	Asn	Gly	Ile	Ala	His	His	Asp	Asn	340	345	350
Ala	Val	Leu	Ile	Thr	Arg	Tyr	Asp	Ile	Cys	Thr	Tyr	Lys	Asn	Lys	Pro	355	360	365
Cys	Gly	Thr	Leu	Gly	Leu	Ala	Ser	Val	Ala	Gly	Met	Cys	Glu	Pro	Glu	370	375	380
Arg	Ser	Cys	Ser	Ile	Asn	Glu	Asp	Ile	Gly	Leu	Gly	Ser	Ala	Phe	Thr	385	390	395
Ile	Ala	His	Glu	Ile	Val	His	Asn	Phe	Gly	Met	Asn	His	Asp	Gly	Ile	405	410	415
Gly	Asn	Ser	Cys	Gly	Arg	Lys	Val	Met	Lys	Gln	Gln	Asn	Tyr	Gly	Ser	420	425	430
Ser	His	Tyr	Cys	Glu	Tyr	Gln	Ser	Phe	Phe	Leu	Val	Cys	Leu	Gln	Ser	435	440	445
Arg	Xaa	His	His	Gln	Leu	Phe	Arg	Glu	Val	Cys	Arg	Glu	Leu	Trp	Cys	450	455	460
Leu	Ser	Lys	Ser	Asn	Arg	Cys	Val	Thr	Asn	Ser	Ile	Pro	Ala	Ala	Glu	465	470	475
Gly	Thr	Leu	Cys	Gln	Thr	Gly	Asn	Ile	Glu	Lys	Gly	Trp	Cys	Tyr	Gln	485	490	495
Gly	Asp	Cys	Val	Pro	Phe	Gly	Thr	Trp	Pro	Gln	Ser	Ile	Asp	Gly	Gly	500	505	510

Cura 468 SEQ list 0405.txt

Trp	Gly	Pro	Trp	Ser	Leu	Trp	Gly	Glu	Cys	Ser	Arg	Thr	Cys	Gly	Gly	
		515					520					525				
Gly	Val	Ser	Ser	Ser	Leu	Arg	His	Cys	Asp	Ser	Pro	Ala	Pro	Ser	Gly	
	530					535					540					
Gly	Gly	Lys	Tyr	Cys	Leu	Gly	Glu	Arg	Lys	Arg	Tyr	Arg	Ser	Cys	Asn	
545					550					555					560	
Thr	Asp	Pro	Cys	Pro	Leu	Gly	Ser	Arg	Asp	Phe	Arg	Glu	Lys	Gln	Cys	
				565					570					575		
Ala	Asp	Phe	Asp	Asn	Met	Pro	Phe	Arg	Gly	Lys	Tyr	Tyr	Asn	Trp	Lys	
			580					585					590			
Pro	Tyr	Thr	Gly	Gly	Gly	Val	Lys	Pro	Cys	Ala	Leu	Asn	Cys	Leu	Ala	
		595					600					605				
Glu	Gly	Tyr	Asn	Phe	Tyr	Thr	Glu	Arg	Ala	Pro	Ala	Val	Ile	Asp	Gly	
	610					615					620					
Thr	Gln	Cys	Asn	Ala	Asp	Ser	Leu	Asp	Ile	Cys	Ile	Asn	Gly	Glu	Cys	
625					630					635					640	
Lys	His	Val	Gly	Cys	Asp	Asn	Ile	Leu	Gly	Ser	Asp	Ala	Arg	Glu	Asp	
				645					650					655		
Arg	Cys	Arg	Val	Cys	Gly	Gly	Gly	Gly	Ser	Thr	Cys	Asp	Ala	Ile	Glu	
			660				665						670			
Gly	Phe	Phe	Asn	Asp	Ser	Leu	Pro	Arg	Gly	Gly	Tyr	Met	Glu	Val	Val	
		675					680					685				
Gln	Ile	Pro	Arg	Gly	Ser	Val	His	Ile	Glu	Val	Arg	Glu	Val	Ala	Met	
	690					695					700					
Ser	Lys	Asn	Tyr	Ile	Ala	Leu	Lys	Ser	Glu	Gly	Asp	Asp	Tyr	Tyr	Ile	
705					710					715					720	
Asn	Gly	Ala	Trp	Thr	Ile	Asp	Trp	Pro	Arg	Lys	Phe	Asp	Val	Ala	Gly	
				725					730					735		
Thr	Ala	Phe	His	Tyr	Lys	Arg	Pro	Thr	Asp	Glu	Pro	Glu	Ser	Leu	Glu	
			740					745					750			
Ala	Leu	Gly	Pro	Thr	Ser	Glu	Asn	Leu	Ile	Val	Met	Val	Leu	Leu	Gln	
		755					760					765				

Cura 468 SEQ list 0405.txt

Glu	Gln	Asn	Leu	Gly	Ile	Arg	Tyr	Lys	Phe	Asn	Val	Pro	Ile	Thr	Arg
770						775					780				
Thr	Gly	Ser	Gly	Asp	Asn	Glu	Val	Gly	Phe	Thr	Trp	Asn	His	Gln	Pro
785					790					795					800
Trp	Ser	Glu	Cys	Ser	Ala	Thr	Cys	Ala	Gly	Gly	Lys	Met	Pro	Thr	Arg
			805						810					815	
Gln	Pro	Thr	Gln	Arg	Ala	Arg	Trp	Arg	Thr	Lys	His	Ile	Leu	Ser	Tyr
			820					825					830		
Ala	Leu	Cys	Leu	Leu	Lys	Lys	Leu	Ile	Gly	Asn	Ile	Ser	Cys	Arg	Phe
		835					840					845			
Ala	Ser	Ser	Cys	Asn	Leu	Ala	Lys	Glu	Thr	Leu	Leu				
	850					855					860				

<210> 35  
 <211> 936  
 <212> PRT  
 <213> Homo sapiens

<400> 35															
Arg	Leu	Leu	Ile	Tyr	Ala	Val	Leu	Pro	Thr	Gly	Asp	Val	Ile	Gly	Asp
1				5					10					15	
Ser	Ala	Lys	Tyr	Asp	Val	Glu	Asn	Cys	Leu	Ala	Asn	Lys	Val	Asp	Leu
			20					25					30		
Ser	Phe	Ser	Pro	Ser	Gln	Ser	Leu	Pro	Ala	Ser	His	Ala	His	Leu	Arg
		35					40					45			
Val	Thr	Ala	Ala	Pro	Gln	Ser	Val	Cys	Ala	Leu	Arg	Ala	Val	Asp	Gln
	50					55					60				
Ser	Val	Leu	Leu	Met	Lys	Pro	Asp	Ala	Glu	Leu	Ser	Ala	Ser	Ser	Val
65					70					75					80
Tyr	Asn	Leu	Leu	Pro	Glu	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gly	Pro	Leu
				85					90					95	
Asn	Asp	Gln	Asp	Asn	Glu	Asp	Cys	Ile	Asn	Arg	His	Asn	Val	Tyr	Ile
		100						105					110		
Asn	Gly	Ile	Thr	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Asn	Glu	Lys	Asp	Met

## Cura 468 SEQ list 0405.txt

115			120			125									
Tyr	Ser	Phe	Leu	Glu	Asp	Met	Gly	Leu	Lys	Ala	Phe	Thr	Asn	Ser	Lys
	130					135					140				
Ile	Arg	Lys	Pro	Lys	Met	Cys	Pro	Gln	Leu	Gln	Gln	Tyr	Glu	Met	His
145					150					155					160
Gly	Pro	Glu	Gly	Leu	Arg	Val	Gly	Phe	Tyr	Glu	Ser	Asp	Val	Met	Gly
				165					170					175	
Arg	Gly	His	Ala	Arg	Leu	Val	His	Val	Glu	Glu	Pro	His	Thr	Glu	Thr
			180					185					190		
Val	Arg	Lys	Tyr	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val
		195					200					205			
Asn	Ser	Ala	Gly	Val	Ala	Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile
		210				215					220				
Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu
225					230					235					240
Gly	Ile	Ser	Ser	Thr	Ala	Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val
				245					250					255	
Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu
			260					265					270		
Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val
		275					280					285			
Gln	Leu	Glu	Ala	Ser	Pro	Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu
	290					295					300				
Gln	Ala	Pro	His	Cys	Ile	Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp
305					310					315					320
Ala	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala
				325					330					335	
Glu	Ala	Leu	Glu	Ser	Gln	Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val
			340					345					350		
Pro	Glu	His	Gly	Arg	Lys	Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu
		355					360					365			
Pro	Glu	Gly	Leu	Glu	Lys	Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro



## Cura 468 SEQ list 0405.txt

370

375

380

Ser 385	Gly	Gly	Glu	Val	Ser 390	Glu	Glu	Leu	Ser	Leu 395	Lys	Leu	Pro	Pro	Asn 400
Val	Val	Glu	Glu	Ser 405	Ala	Arg	Ala	Ser	Val 410	Ser	Val	Leu	Gly	Asp 415	Ile
Leu	Gly	Ser	Ala 420	Met	Gln	Asn	Thr	Gln 425	Asn	Leu	Leu	Gln	Met 430	Pro	Tyr
Gly	Cys	Gly 435	Glu	Gln	Asn	Met	Val 440	Leu	Phe	Ala	Pro	Asn 445	Ile	Tyr	Val
Leu	Asp 450	Tyr	Leu	Asn	Glu	Thr 455	Gln	Gln	Leu	Thr	Pro 460	Glu	Ile	Lys	Ser
Lys 465	Ala	Ile	Gly	Tyr	Leu 470	Asn	Thr	Gly	Tyr	Gln 475	Arg	Gln	Leu	Asn 480	Tyr
Lys	His	Tyr	Asp	Gly 485	Ser	Tyr	Ser	Thr	Phe 490	Gly	Glu	Arg	Tyr	Gly 495	Arg
Asn	Gln	Gly	Asn 500	Thr	Trp	Leu	Thr	Ala 505	Phe	Val	Leu	Lys	Thr 510	Phe	Ala
Gln	Ala	Arg	Ala 515	Tyr	Ile	Phe	Ile 520	Asp	Glu	Ala	His	Ile 525	Thr	Gln	Ala
Leu 530	Ile	Trp	Leu	Ser	Gln	Arg 535	Gln	Lys	Asp	Asn	Gly 540	Cys	Phe	Arg	Ser
Ser 545	Gly	Ser	Leu	Leu	Asn 550	Asn	Ala	Ile	Lys	Gly 555	Gly	Val	Glu	Asp	Glu 560
Val	Thr	Leu	Ser	Ala 565	Tyr	Ile	Thr	Ile	Ala 570	Leu	Leu	Glu	Ile	Pro 575	Leu
Thr	Val	Thr	His 580	Pro	Val	Val	Arg	Asn 585	Ala	Leu	Phe	Cys	Leu 590	Glu	Ser
Ala	Trp	Lys	Thr 595	Ala	Gln	Glu	Gly 600	Asp	His	Gly	Ser	His 605	Val	Tyr	Thr
Lys 610	Ala	Leu	Leu	Ala	Tyr	Ala 615	Phe	Ala	Leu	Ala	Gly 620	Asn	Gln	Asp	Lys
Arg	Lys	Glu	Val	Leu	Lys	Ser	Leu	Asn	Glu	Glu	Ala	Val	Lys	Lys	Asp

## Cura 468 SEQ list 0405.txt

625																
Asn	Ser	Val	His	Trp	Glu	Arg	Pro	Gln	Lys	Pro	Lys	Ala	Pro	Val	Gly	
				645					650					655		
His	Phe	Tyr	Glu	Pro	Gln	Ala	Pro	Ser	Ala	Glu	Val	Glu	Met	Thr	Ser	
			660					665					670			
Tyr	Val	Leu	Leu	Ala	Tyr	Leu	Thr	Ala	Gln	Pro	Ala	Pro	Thr	Ser	Glu	
		675					680					685				
Asp	Leu	Thr	Ser	Ala	Thr	Asn	Ile	Val	Lys	Trp	Ile	Thr	Lys	Gln	Gln	
	690					695					700					
Asn	Ala	Gln	Gly	Gly	Phe	Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu	
705					710					715					720	
His	Ala	Leu	Ser	Lys	Tyr	Gly	Ala	Ala	Thr	Phe	Thr	Arg	Thr	Gly	Lys	
				725					730					735		
Ala	Ala	Gln	Val	Thr	Ile	Gln	Ser	Ser	Gly	Thr	Phe	Ser	Ser	Lys	Phe	
			740					745					750			
Gln	Val	Asp	Asn	Asn	Asn	Arg	Leu	Leu	Leu	Gln	Gln	Val	Ser	Leu	Pro	
		755					760					765				
Glu	Leu	Pro	Gly	Glu	Tyr	Ser	Met	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val	
	770					775					780					
Tyr	Leu	Gln	Thr	Ser	Leu	Lys	Tyr	Asn	Ile	Leu	Pro	Glu	Lys	Glu	Glu	
785					790					795					800	
Phe	Pro	Phe	Ala	Leu	Gly	Val	Gln	Thr	Leu	Pro	Gln	Thr	Cys	Asp	Glu	
				805					810					815		
Pro	Lys	Ala	His	Thr	Ser	Phe	Gln	Ile	Ser	Leu	Ser	Val	Ser	Tyr	Thr	
			820					825					830			
Gly	Ser	Arg	Ser	Ala	Ser	Asn	Met	Ala	Ile	Val	Asp	Val	Lys	Met	Val	
		835					840					845				
Ser	Gly	Phe	Ile	Pro	Leu	Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser	
	850					855					860					
Asn	His	Val	Ser	Arg	Thr	Glu	Val	Ser	Ser	Asn	His	Val	Leu	Ile	Tyr	
865					870					875					880	
Leu	Asp	Lys	Val	Ser	Asn	Gln	Thr	Leu	Ser	Leu	Phe	Phe	Thr	Val	Leu	

## Cura 468 SEQ list 0405.txt

885

890

895

Gln Asp Val Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr  
                   900                                  905                                  910

Asp Tyr Tyr Glu Thr Gly Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro  
                   915                                  920                                  925

Cys Ser Lys Asp Leu Gly Asn Ala  
           930                                  935

&lt;210&gt; 36

&lt;211&gt; 898

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 36

Arg Leu Leu Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp  
   1                                  5                                  10                                  15

Ser Ala Lys Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu  
                   20                                  25                                  30

Ser Phe Ser Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg  
           35                                  40                                  45

Val Thr Ala Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln  
   50                                  55                                  60

Ser Val Leu Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val  
   65                                  70                                  75                                  80

Tyr Asn Leu Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu  
                   85                                  90                                  95

Asn Asp Gln Asp Asp Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile  
                   100                                  105                                  110

Asn Gly Ile Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met  
           115                                  120                                  125

Tyr Ser Phe Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys  
   130                                  135                                  140

Ile Arg Lys Glu Glu Pro His Thr Glu Thr Val Arg Lys Tyr Phe Pro  
  145                                  150                                  155                                  160

Cura 468 SEQ list 0405.txt

Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val	Asn	Ser	Ala	Gly	Val	Ala
				165					170					175	
Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile	Thr	Glu	Trp	Lys	Ala	Gly
			180					185					190		
Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu	Gly	Ile	Ser	Ser	Thr	Ala
		195					200					205			
Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro	Tyr
	210					215					220				
Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu	Asn
225					230					235					240
Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val	Gln	Leu	Glu	Ala	Ser	Pro
				245					250					255	
Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu	Gln	Ala	Pro	His	Cys	Ile
			260					265					270		
Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp	Ala	Val	Thr	Pro	Lys	Ser
		275					280					285			
Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Glu	Ser	Gln
	290					295					300				
Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val	Pro	Glu	His	Gly	Arg	Lys
305					310					315					320
Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu	Pro	Glu	Gly	Leu	Glu	Lys
				325					330					335	
Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	Ser	Gly	Gly	Glu	Val	Ser
			340					345					350		
Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn	Val	Val	Glu	Glu	Ser	Ala
		355					360					365			
Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met	Gln
	370					375					380				
Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn
385					390					395					400
Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn	Glu
				405					410					415	

Cura 468 SEQ list 0405.txt

Thr	Gln	Gln	Leu	Thr	Pro	Glu	Val	Lys	Ser	Lys	Ala	Ile	Gly	Tyr	Leu	
			420					425					430			
Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Lys	His	Tyr	Asp	Gly	Ser	
		435					440					445				
Tyr	Ser	Thr	Phe	Gly	Glu	Arg	Tyr	Gly	Arg	Asn	Gln	Gly	Asn	Thr	Trp	
	450					455					460					
Leu	Thr	Ala	Phe	Val	Leu	Lys	Thr	Phe	Ala	Gln	Ala	Arg	Ala	Tyr	Ile	
465					470					475					480	
Phe	Ile	Asp	Glu	Ala	His	Ile	Thr	Gln	Ala	Leu	Ile	Trp	Leu	Ser	Gln	
				485					490					495		
Arg	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser	Ser	Gly	Ser	Leu	Leu	Asn	
			500					505					510			
Asn	Ala	Ile	Lys	Gly	Gly	Val	Glu	Asp	Glu	Val	Thr	Leu	Ser	Ala	Tyr	
		515					520					525				
Ile	Thr	Ile	Ala	Leu	Leu	Glu	Ile	Pro	Leu	Thr	Val	Thr	His	Pro	Val	
	530					535					540					
Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Glu	Ser	Ala	Trp	Lys	Thr	Ala	Gln	
545					550					555					560	
Glu	Gly	Asp	His	Gly	Ser	His	Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	
				565					570					575		
Ala	Phe	Ala	Leu	Ala	Gly	Asn	Gln	Asp	Lys	Arg	Lys	Glu	Val	Leu	Lys	
			580					585					590			
Ser	Leu	Asn	Glu	Glu	Ala	Val	Lys	Lys	Asp	Asn	Ser	Val	His	Trp	Glu	
		595					600					605				
Arg	Pro	Gln	Lys	Pro	Lys	Ala	Pro	Val	Gly	His	Phe	Tyr	Glu	Pro	Gln	
	610					615					620					
Ala	Pro	Ser	Ala	Glu	Val	Glu	Met	Thr	Ser	Tyr	Val	Leu	Leu	Ala	Tyr	
625					630					635					640	
Leu	Thr	Ala	Gln	Pro	Ala	Pro	Thr	Ser	Glu	Asp	Leu	Thr	Ser	Ala	Thr	
				645					650					655		
Asn	Ile	Val	Lys	Trp	Ile	Thr	Lys	Gln	Gln	Asn	Ala	Gln	Gly	Gly	Phe	
			660					665					670			

Cura 468 SEQ list 0405.txt

Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys	Tyr
		675					680					685			
Gly	Ala	Ala	Thr	Phe	Thr	Arg	Thr	Gly	Lys	Ala	Ala	Gln	Val	Thr	Ile
	690					695					700				
Gln	Ser	Ser	Gly	Thr	Phe	Ser	Ser	Lys	Phe	Gln	Val	Asp	Asn	Asn	Asn
705					710					715					720
Arg	Leu	Leu	Leu	Gln	Gln	Val	Ser	Leu	Pro	Glu	Leu	Pro	Gly	Glu	Tyr
				725					730					735	
Ser	Met	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val	Tyr	Leu	Gln	Thr	Ser	Leu
			740					745					750		
Lys	Tyr	Asn	Ile	Leu	Pro	Glu	Lys	Glu	Glu	Phe	Pro	Phe	Ala	Leu	Gly
		755					760					765			
Val	Gln	Thr	Leu	Pro	Gln	Thr	Cys	Asp	Glu	Pro	Lys	Ala	His	Thr	Ser
	770					775					780				
Phe	Gln	Ile	Ser	Leu	Ser	Val	Ser	Tyr	Thr	Gly	Ser	Arg	Ser	Ala	Ser
785					790					795					800
Asn	Met	Ala	Ile	Val	Asp	Val	Lys	Met	Val	Ser	Gly	Phe	Ile	Pro	Leu
				805					810					815	
Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser	Asn	His	Val	Ser	Arg	Thr
			820					825					830		
Glu	Val	Ser	Ser	Asn	His	Val	Leu	Ile	Tyr	Leu	Asp	Lys	Val	Ser	Asn
		835					840					845			
Gln	Thr	Leu	Ser	Leu	Phe	Phe	Thr	Val	Leu	Gln	Asp	Val	Pro	Val	Arg
	850					855					860				
Asp	Leu	Lys	Pro	Ala	Ile	Val	Lys	Val	Tyr	Asp	Tyr	Tyr	Glu	Thr	Asp
865					870					875					880
Glu	Phe	Ala	Ile	Ala	Glu	Tyr	Asn	Ala	Pro	Cys	Ser	Lys	Asp	Leu	Gly
				885					890					895	

Asn Ala

<210> 37

<211> 936

Cura 468 SEQ list 0405.txt

<212> PRT

<213> Homo sapiens

<400> 37

Arg	Leu	Leu	Ile	Tyr	Ala	Val	Leu	Pro	Thr	Gly	Asp	Val	Ile	Gly	Asp	
1				5					10					15		
Ser	Ala	Lys	Tyr	Asp	Val	Glu	Asn	Glu	Leu	Ala	Asn	Lys	Val	Asp	Leu	
			20					25					30			
Ser	Phe	Ser	Pro	Ser	Gln	Ser	Leu	Pro	Ala	Ser	His	Ala	His	Leu	Arg	
		35					40					45				
Val	Thr	Ala	Ala	Pro	Gln	Ser	Val	Cys	Ala	Leu	Arg	Ala	Val	Asp	Gln	
	50					55					60					
Ser	Val	Leu	Leu	Met	Lys	Pro	Asp	Ala	Glu	Leu	Ser	Ala	Ser	Ser	Val	
65					70					75					80	
Tyr	Asn	Leu	Leu	Pro	Glu	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gly	Pro	Leu	
				85					90					95		
Asn	Asp	Gln	Asp	Asp	Glu	Asp	Cys	Ile	Asn	Arg	His	Asn	Val	Tyr	Ile	
			100					105					110			
Asn	Gly	Ile	Thr	Tyr	Thr	Pro	Val	Ser	Ser	Thr	Asn	Glu	Lys	Asp	Met	
		115					120					125				
Tyr	Ser	Phe	Leu	Glu	Asp	Met	Gly	Leu	Lys	Ala	Phe	Thr	Asn	Ser	Lys	
	130					135					140					
Ile	Arg	Lys	Pro	Lys	Met	Cys	Pro	Gln	Leu	Gln	Gln	Tyr	Glu	Met	His	
145					150					155					160	
Gly	Pro	Glu	Gly	Leu	Arg	Val	Gly	Phe	Tyr	Glu	Ser	Asp	Val	Met	Gly	
			165						170					175		
Arg	Gly	His	Ala	Arg	Leu	Val	His	Val	Glu	Glu	Pro	His	Thr	Glu	Thr	
			180					185					190			
Val	Arg	Lys	Tyr	Phe	Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val	
		195					200					205				
Asn	Ser	Ala	Gly	Val	Ala	Glu	Val	Gly	Val	Thr	Val	Pro	Asp	Thr	Ile	
	210					215					220					
Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser	Glu	Asp	Ala	Gly	Leu	
225					230					235					240	

Cura 468 SEQ list 0405.txt

Gly	Ile	Ser	Ser	Thr	Ala	Ser	Leu	Arg	Ala	Phe	Gln	Pro	Phe	Phe	Val	
				245					250					255		
Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	
			260					265					270			
Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Lys	Cys	Ile	Arg	Val	Ser	Val	
		275					280					285				
Gln	Leu	Glu	Ala	Ser	Pro	Ala	Phe	Leu	Ala	Val	Pro	Val	Glu	Lys	Glu	
	290					295					300					
Gln	Ala	Pro	His	Cys	Ile	Cys	Ala	Asn	Gly	Arg	Gln	Thr	Val	Ser	Trp	
305					310					315					320	
Ala	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala	
				325					330					335		
Glu	Ala	Leu	Glu	Ser	Gln	Glu	Leu	Cys	Gly	Thr	Glu	Val	Pro	Ser	Val	
			340					345					350			
Pro	Glu	His	Gly	Arg	Lys	Asp	Thr	Val	Ile	Lys	Pro	Leu	Leu	Val	Glu	
		355					360					365				
Pro	Glu	Gly	Leu	Glu	Lys	Glu	Thr	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	
	370					375					380					
Ser	Gly	Gly	Glu	Val	Ser	Glu	Glu	Leu	Ser	Leu	Lys	Leu	Pro	Pro	Asn	
385					390					395					400	
Val	Val	Glu	Glu	Ser	Ala	Arg	Ala	Ser	Val	Ser	Val	Leu	Gly	Asp	Ile	
				405					410					415		
Leu	Gly	Ser	Ala	Met	Gln	Asn	Thr	Gln	Asn	Leu	Leu	Gln	Met	Pro	Tyr	
			420					425					430			
Gly	Cys	Gly	Glu	Glx	Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val	
		435					440					445				
Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	Thr	Pro	Glu	Ile	Lys	Ser	
	450					455					460					
Lys	Ala	Ile	Gly	Tyr	Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	
465					470					475					480	
Lys	His	Tyr	Asp	Gly	Ser	Tyr	Ser	Thr	Phe	Gly	Glu	Arg	Tyr	Gly	Arg	
				485					490					495		



Cura 468 SEQ list 0405.txt

Asn	Gln	Gly	Asn	Thr	Trp	Leu	Thr	Ala	Phe	Val	Leu	Lys	Thr	Phe	Ala	500	505	510	
Gln	Ala	Arg	Ala	Tyr	Ile	Phe	Ile	Asp	Glu	Ala	His	Ile	Thr	Gln	Ala	515	520	525	
Leu	Ile	Trp	Leu	Ser	Gln	Arg	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser	530	535	540	
Ser	Gly	Ser	Leu	Leu	Asn	Asn	Ala	Ile	Lys	Gly	Gly	Val	Glu	Asp	Glu	545	550	555	560
Val	Thr	Leu	Ser	Ala	Tyr	Ile	Lys	Ile	Ala	Leu	Leu	Glu	Ile	Pro	Leu	565	570	575	
Thr	Val	Thr	His	Pro	Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Glu	Ser	580	585	590	
Ala	Trp	Lys	Thr	Ala	Glu	Glu	Gly	Asp	His	Gly	Ser	His	Val	Tyr	Thr	595	600	605	
Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Asn	Gln	Asp	Lys	610	615	620	
Arg	Lys	Glu	Val	Leu	Lys	Ser	Leu	Asn	Glu	Glu	Ala	Val	Lys	Lys	Asp	625	630	635	640
Asn	Ser	Val	His	Trp	Glu	Arg	Pro	Gln	Lys	Pro	Lys	Ala	Pro	Val	Gly	645	650	655	
His	Phe	Tyr	Glu	Pro	Gln	Ala	Pro	Ser	Ala	Glu	Val	Glu	Met	Thr	Ser	660	665	670	
Tyr	Val	Leu	Leu	Ala	Tyr	Leu	Thr	Ala	Gln	Pro	Ala	Pro	Thr	Ser	Glu	675	680	685	
Asp	Leu	Thr	Ser	Ala	Thr	Asn	Ile	Val	Lys	Trp	Ile	Thr	Lys	Gln	Gln	690	695	700	
Asn	Ala	Gln	Gly	Gly	Phe	Ser	Ser	Thr	Gln	Asp	Lys	Val	Val	Ala	Leu	705	710	715	720
His	Ala	Leu	Ser	Lys	Tyr	Gly	Ala	Ala	Thr	Phe	Thr	Arg	Thr	Gly	Lys	725	730	735	
Ala	Ala	Gln	Val	Thr	Ile	Gln	Ser	Ser	Gly	Thr	Phe	Ser	Ser	Lys	Phe	740	745	750	

Cura 468 SEQ list 0405.txt

Gln	Val	Asp	Asn	Asn	Asn	Arg	Leu	Leu	Leu	Gln	Gln	Val	Ser	Leu	Pro
		755					760					765			
Glu	Leu	Pro	Gly	Glu	Tyr	Ser	Met	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val
		770				775					780				
Tyr	Leu	Gln	Thr	Ser	Leu	Lys	Tyr	Asn	Ile	Leu	Pro	Glu	Lys	Glu	Glu
785					790					795					800
Phe	Pro	Phe	Ala	Leu	Gly	Val	Gln	Thr	Leu	Pro	Gln	Thr	Cys	Asp	Glu
				805					810					815	
Pro	Lys	Ala	His	Thr	Ser	Phe	Gln	Ile	Ser	Leu	Ser	Val	Ser	Tyr	Thr
			820					825					830		
Gly	Ser	Arg	Ser	Ala	Ser	Asn	Met	Ala	Ile	Val	Asp	Val	Lys	Met	Val
		835					840					845			
Ser	Gly	Phe	Ile	Pro	Leu	Lys	Pro	Thr	Val	Lys	Met	Leu	Glu	Arg	Ser
	850					855					860				
Asn	His	Val	Ser	Arg	Thr	Glu	Val	Ser	Ser	Asn	His	Val	Leu	Ile	Tyr
865					870					875					880
Leu	Asp	Lys	Val	Ser	Asn	Gln	Thr	Leu	Ser	Leu	Phe	Phe	Thr	Val	Leu
				885					890					895	
Gln	Asp	Val	Pro	Val	Arg	Asp	Leu	Lys	Pro	Ala	Ile	Val	Lys	Val	Tyr
			900					905					910		
Asp	Tyr	Tyr	Glu	Thr	Asp	Glu	Phe	Ala	Ile	Ala	Glu	Tyr	Asn	Ala	Pro
		915					920					925			
Cys	Ser	Lys	Asp	Leu	Gly	Asn	Ala								
	930					935									

<210> 38

<211> 931

<212> PRT

<213> Rattus norvegicus

<400> 38

Arg	Leu	Val	Leu	Tyr	Ala	Ile	Leu	Pro	Asn	Gly	Glu	Val	Val	Gly	Asp
1				5					10					15	

Thr	Ala	Lys	Tyr	Glu	Ile	Glu	Asn	Cys	Leu	Ala	Asn	Lys	Val	Asp	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## Cura 468 SEQ list 0405.txt

20

25

30

Val	Phe	Arg	Pro	Asn	Ser	Gly	Leu	Pro	Ala	Thr	Arg	Ala	Leu	Leu	Ser
		35					40					45			
Val	Met	Ala	Ser	Pro	Gln	Ser	Leu	Cys	Gly	Leu	Arg	Ala	Val	Asp	Gln
	50					55					60				
Ser	Val	Leu	Leu	Met	Lys	Pro	Glu	Thr	Glu	Leu	Ser	Ala	Ser	Leu	Ile
65					70					75					80
Tyr	Asp	Leu	Leu	Pro	Val	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gln	Gly	Ala
				85					90					95	
Asp	Gln	Arg	Glu	Glu	Asp	Thr	Asn	Gly	Cys	Val	Lys	Gln	Asn	Asp	Thr
			100					105					110		
Tyr	Ile	Asn	Gly	Ile	Leu	Tyr	Ser	Pro	Val	Gln	Asn	Thr	Asn	Glu	Glu
		115					120					125			
Asp	Met	Tyr	Gly	Phe	Leu	Lys	Asp	Met	Gly	Leu	Lys	Val	Phe	Thr	Asn
	130					135					140				
Ser	Asn	Ile	Arg	Lys	Pro	Lys	Val	Cys	Glu	Arg	Leu	Arg	Asp	Asn	Lys
145					150					155					160
Gly	Ile	Pro	Ala	Ala	Tyr	His	Leu	Val	Ser	Gln	Ser	His	Met	Asp	Ala
				165					170					175	
Phe	Leu	Glu	Ser	Ser	Glu	Ser	Pro	Thr	Glu	Thr	Arg	Arg	Ser	Tyr	Phe
			180					185					190		
Pro	Glu	Thr	Trp	Ile	Trp	Asp	Leu	Val	Val	Val	Asp	Ser	Ala	Gly	Val
		195					200					205			
Ala	Glu	Val	Glu	Val	Thr	Val	Pro	Asp	Thr	Ile	Thr	Glu	Trp	Lys	Ala
	210					215					220				
Gly	Ala	Phe	Cys	Leu	Ser	Asn	Asp	Thr	Gly	Leu	Gly	Leu	Ser	Pro	Val
225					230					235					240
Val	Gln	Phe	Gln	Ala	Phe	Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro
				245					250					255	
Tyr	Ser	Val	Ile	Arg	Gly	Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu
			260				265						270		
Asn	Tyr	Leu	Pro	Thr	Cys	Ile	Arg	Val	Ala	Val	Gln	Leu	Glu	Ala	Ser

## Cura 468 SEQ list 0405.txt

275					280					285					
Pro	Asp	Phe	Leu	Ala	Ala	Pro	Glu	Glu	Lys	Glu	Gln	Arg	Ser	His	Cys
	290					295					300				
Ile	Cys	Met	Asn	Gln	Arg	His	Thr	Ala	Ser	Trp	Ala	Val	Ile	Pro	Lys
305					310					315					320
Ser	Leu	Gly	Asn	Val	Asn	Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Asn	Ser
				325					330					335	
Lys	Glu	Leu	Cys	Gly	Asn	Glu	Val	Pro	Val	Val	Pro	Glu	Gln	Gly	Lys
			340					345					350		
Lys	Asp	Thr	Ile	Ile	Lys	Ser	Leu	Leu	Val	Glu	Pro	Glu	Gly	Leu	Glu
		355					360					365			
Asn	Glu	Val	Thr	Phe	Asn	Ser	Leu	Leu	Cys	Pro	Met	Gly	Ala	Glu	Val
	370					375					380				
Ser	Glu	Leu	Ile	Ala	Leu	Lys	Leu	Pro	Ser	Asp	Val	Val	Glu	Glu	Ser
385					390					395					400
Ala	Arg	Ala	Ser	Val	Thr	Val	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met
				405					410					415	
Gln	Asn	Thr	Gln	Asp	Leu	Leu	Lys	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln
			420					425					430		
Asn	Met	Val	Leu	Phe	Ala	Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn
		435					440					445			
Glu	Thr	Gln	Gln	Leu	Thr	Gln	Glu	Ile	Lys	Thr	Lys	Ala	Ile	Ala	Tyr
	450					455					460				
Leu	Asn	Thr	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Lys	His	Arg	Asp	Gly
465					470					475					480
Ser	Tyr	Ser	Ala	Phe	Gly	Asp	Lys	Pro	Gly	Arg	Asn	His	Ala	Asn	Thr
				485					490					495	
Trp	Leu	Thr	Ala	Phe	Val	Leu	Lys	Ser	Phe	Ala	Gln	Ala	Arg	Lys	Tyr
			500					505					510		
Ile	Phe	Ile	Asp	Glu	Val	His	Ile	Thr	Gln	Ala	Leu	Leu	Trp	Leu	Ser
		515					520					525			
Gln	Gln	Gln	Lys	Asp	Asn	Gly	Cys	Phe	Arg	Ser	Ser	Gly	Ser	Leu	Leu

## Cura 468 SEQ list 0405.txt

530																
Asn	Asn	Ala	Met	Lys	Gly	Gly	Val	Glu	Asp	Glu	Val	Thr	Leu	Ser	Ala	
545					550					555					560	
Tyr	Ile	Thr	Ile	Ala	Leu	Leu	Glu	Met	Ser	Leu	Pro	Val	Thr	His	Pro	
				565					570					575		
Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	Leu	Asp	Thr	Ala	Trp	Lys	Ser	Ala	
			580					585					590			
Arg	Gly	Gly	Ala	Gly	Gly	Ser	His	Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	
		595					600					605				
Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Pro	Val	Val	Arg	Asn	Ala	Leu	Phe	Cys	
	610					615					620					
Leu	Asp	Thr	Ala	Trp	Lys	Ser	Ala	Arg	Gly	Gly	Ala	Gly	Gly	Ser	His	
625					630					635					640	
Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	Gly	Pro	
				645					650					655		
Gln	Ala	Thr	Ser	Ala	Glu	Val	Glu	Met	Thr	Ala	Tyr	Val	Leu	Leu	Ala	
			660					665					670			
Tyr	Leu	Thr	Thr	Glu	Pro	Ala	Pro	Thr	Gln	Glu	Asp	Leu	Thr	Ala	Ala	
		675					680					685				
Met	Leu	Ile	Val	Lys	Trp	Leu	Thr	Lys	Gln	Gln	Asn	Ser	His	Gly	Gly	
	690					695					700					
Phe	Ser	Ser	Thr	Gln	Asp	Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys	
705					710					715					720	
Tyr	Gly	Ser	Ala	Thr	Phe	Thr	Arg	Ala	Lys	Lys	Ala	Ala	Gln	Val	Thr	
				725					730					735		
Ile	Arg	Ser	Ser	Gly	Thr	Phe	Ser	Thr	Lys	Phe	Gln	Val	Asn	Asn	Asn	
			740					745					750			
Asn	Gln	Leu	Leu	Leu	Gln	Arg	Val	Thr	Leu	Pro	Thr	Val	Pro	Gly	Asp	
		755					760					765				
Tyr	Thr	Val	Lys	Val	Thr	Gly	Glu	Gly	Cys	Val	Tyr	Leu	Gln	Thr	Ser	
	770					775					780					
Leu	Lys	Tyr	Ser	Val	Leu	Pro	Arg	Glu	Glu	Glu	Phe	Pro	Phe	Ala	Val	

Cura 468 SEQ list 0405.txt

785 790 795 800

Val Val Gln Thr Leu Pro Gly Thr Cys Glu Asp Pro Lys Ala His Thr  
805 810 815

Ser Phe Gln Ile Ser Leu Asn Ile Ser Tyr Thr Gly Ser Arg Ser Glu  
820 825 830

Ser Asn Met Ala Ile Ala Asp Val Lys Met Val Ser Gly Phe Ile Pro  
835 840 845

Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Val His Val Ser Arg  
850 855 860

Thr Glu Val Ser Asn Asn His Val Leu Ile Tyr Leu Asp Lys Val Ser  
865 870 875 880

Asn Gln Thr Val Asn Leu Ser Phe Thr Val Gln Gln Asp Ile Pro Ile  
885 890 895

Arg Asp Leu Lys Pro Ala Val Val Lys Val Tyr Asp Tyr Tyr Glu Lys  
900 905 910

Asp Glu Phe Ala Val Ala Lys Tyr Ser Ala Pro Cys Ser Thr Asp Tyr  
915 920 925

Gly Asn Ala  
930

<210> 39

<211> 941

<212> PRT

<213> Cavia porcellus

<400> 39

Arg Val Leu Ile Tyr Ala Ile Leu Pro Ser Gly Glu Ile Ile Ala Asp  
1 5 10 15

Ser Ala Lys Tyr Asn Val Glu Asn Cys Leu Asp Asn Lys Val Asn Leu  
20 25 30

Ser Phe Ser Glu Gly Gln Ser Leu Pro Ala Ser Lys Thr His Leu Arg  
35 40 45

Val Thr Ala Ser Pro Gln Ser Leu Cys Ala Leu Arg Ala Val Asp Gln  
50 55 60

## Cura 468 SEQ list 0405.txt

Ser	Val	Leu	Leu	Arg	Lys	Pro	Glu	Ala	Val	Leu	Ser	Ala	Ser	Ser	Val	65	70	75	80
Tyr	Ala	Leu	Leu	Pro	Val	Lys	Asp	Leu	Thr	Gly	Phe	Pro	Gly	Leu	Leu		85	90	95
Gly	Gln	Gln	Glu	Glu	Asn	Asp	Gly	Glu	Cys	Val	Ser	Leu	Tyr	Asn	Thr		100	105	110
Tyr	Ile	Asp	Gly	Ile	Leu	Tyr	Ser	Pro	Glu	Pro	Asn	Ile	Asn	Glu	Lys		115	120	125
Asp	Met	Tyr	Gly	Phe	Leu	Lys	Asp	Met	Gly	Leu	Lys	Val	Phe	Thr	Asn		130	135	140
Thr	Lys	Ile	Gln	Lys	Pro	Gln	Leu	Cys	Ala	His	Val	Gln	Lys	Phe	Glu		145	150	155
Val	Pro	Thr	Met	Ala	Tyr	Ser	Tyr	Ser	Glu	Ser	Ser	Ser	Phe	Arg	Ser		165	170	175
Gly	Pro	Arg	Arg	Val	Pro	Ala	Val	Gly	Ile	Ala	Ala	Thr	Tyr	Ser	Glu		180	185	190
Pro	Pro	Lys	Glu	Thr	Val	Arg	Thr	Tyr	Ser	Pro	Glu	Thr	Trp	Ile	Trp		195	200	205
Asp	Leu	Lys	Val	Thr	Asp	Ser	Ser	Gly	Val	Ala	Glu	Val	Glu	Val	Thr		210	215	220
Val	Pro	Asp	Thr	Ile	Thr	Glu	Trp	Lys	Ala	Gly	Ala	Phe	Cys	Leu	Ser		225	230	235
Asn	Asp	Thr	Gly	Leu	Gly	Leu	Ser	Pro	Thr	Ala	Ser	Leu	Arg	Ala	Phe		245	250	255
Gln	Pro	Phe	Phe	Val	Glu	Leu	Thr	Met	Pro	Tyr	Ser	Val	Ile	Arg	Gly		260	265	270
Glu	Ala	Phe	Thr	Leu	Lys	Ala	Thr	Val	Leu	Asn	Tyr	Leu	Pro	Asp	Cys		275	280	285
Ile	Arg	Ile	Ser	Val	His	Leu	Glu	Ala	Ser	Pro	Lys	Phe	Leu	Ala	Glu		290	295	300
Pro	Lys	Ala	Lys	Glu	Gln	Glu	Ser	Tyr	Cys	Val	Cys	Gly	Asn	Glu	Arg		305	310	315
																			320

## Cura 468 SEQ list 0405.txt

Gln	Thr	Val	Ser	Trp	Val	Val	Thr	Pro	Lys	Ser	Leu	Gly	Asn	Val	Asn
				325					330					335	
Phe	Thr	Val	Ser	Ala	Glu	Ala	Leu	Glu	Ser	Ser	Glu	Leu	Cys	Gly	Asn
			340					345					350		
Glu	Lys	Thr	Val	Val	Pro	Thr	Tyr	Gly	Lys	Lys	Asp	Thr	Ile	Ile	Lys
		355					360					365			
Pro	Leu	Leu	Val	Glu	Pro	Glu	Gly	Ile	Glu	Lys	Glu	Glu	Thr	Trp	Thr
	370					375					380				
Ser	Leu	Ile	Arg	Val	Ser	Asp	Thr	Thr	Val	Ser	Glu	Lys	Leu	His	Leu
385					390					395					400
Glu	Leu	Pro	Ser	Asn	Val	Ile	Gln	Asp	Ser	Ala	Arg	Ala	Thr	Val	Ser
				405					410					415	
Ile	Leu	Gly	Asp	Ile	Leu	Gly	Ser	Ala	Met	Gln	Asn	Ile	Gln	Asn	Leu
			420					425					430		
Leu	Gln	Met	Pro	Tyr	Gly	Cys	Gly	Glu	Gln	Asn	Met	Val	Leu	Phe	Ala
		435					440					445			
Pro	Asn	Ile	Tyr	Val	Leu	Asp	Tyr	Leu	Asn	Glu	Thr	Gln	Gln	Leu	Thr
	450					455					460				
Pro	Asp	Ile	Lys	Ser	Lys	Ala	Ile	Ser	Tyr	Leu	Ser	Thr	Gly	Tyr	Gln
465					470					475					480
Arg	Gln	Leu	Asn	Tyr	Lys	His	Arg	Asp	Gly	Ser	Tyr	Ser	Thr	Phe	Gly
				485					490					495	
Glu	Asn	Tyr	Arg	Gly	Gly	Gln	Gly	Asn	Thr	Trp	Leu	Thr	Ala	Phe	Val
			500					505					510		
Leu	Lys	Thr	Phe	Ser	Gln	Ala	Arg	Lys	Tyr	Ile	Phe	Ile	Asp	Glu	Ala
		515					520					525			
His	Ile	Thr	Gln	Ala	Leu	Ser	Trp	Leu	Ser	Gln	Lys	Gln	Lys	Asp	Asn
	530					535					540				
Gly	Cys	Phe	Trp	Ser	Ser	Gly	Ser	Leu	Leu	Asn	Asn	Ala	Ile	Lys	Gly
545					550					555					560
Gly	Val	Glu	Asp	Glu	Ile	Ser	Leu	Ser	Ala	Tyr	Ile	Thr	Ile	Ala	Leu
				565					570					575	



## Cura 468 SEQ list 0405.txt

Leu	Glu	Met	Ser	Leu	Pro	Asp	Thr	His	Pro	Val	Val	Arg	Asn	Ala	Leu	580	585	590
Phe	Cys	Leu	Glu	Ser	Ala	Trp	Lys	Ser	Ala	Lys	Glu	Gly	Thr	His	Gly	595	600	605
Ser	His	Val	Tyr	Thr	Lys	Ala	Leu	Leu	Ala	Tyr	Ala	Phe	Ala	Leu	Ala	610	615	620
Gly	Asn	Gln	Glu	Arg	Lys	Lys	Glu	Ile	Leu	Lys	Ser	Leu	Glu	Asp	Glu	625	630	635
Gly	Val	Lys	Glu	Asp	Asn	Ser	Leu	His	Trp	Ala	Arg	Pro	Gln	Lys	Pro	645	650	655
Lys	Val	Ser	Glu	Gly	Phe	Leu	Phe	Lys	Ser	Gln	Ala	Pro	Ser	Ala	Glu	660	665	670
Val	Glu	Met	Thr	Ser	Tyr	Val	Leu	Leu	Ala	Tyr	Leu	Thr	Ala	Arg	Pro	675	680	685
Ala	Pro	Thr	Pro	Glu	Asp	Leu	Thr	Ser	Ala	Thr	Asp	Ile	Val	Asn	Trp	690	695	700
Val	Thr	Lys	Gln	Gln	Asn	Ser	His	Gly	Gly	Tyr	Ser	Ser	Thr	Gln	Asp	705	710	715
Thr	Val	Val	Ala	Leu	His	Ala	Leu	Ser	Lys	Tyr	Ala	Ala	Ala	Thr	Phe	725	730	735
Thr	Arg	Thr	Glu	Lys	Ala	Ala	Gln	Val	Thr	Ile	Lys	Ser	Ser	Gly	Thr	740	745	750
Phe	Ser	Thr	Asn	Phe	Glu	Val	Asn	His	Asn	Asn	Arg	Leu	Leu	Leu	Gln	755	760	765
Gln	Val	Ser	Leu	Pro	Thr	Val	Ser	Asp	Ser	Tyr	Thr	Ile	Thr	Val	Thr	770	775	780
Gly	Glu	Gly	Asn	Val	Tyr	Leu	Gln	Thr	Ser	Leu	Lys	Tyr	Asn	Val	Pro	785	790	795
Ser	Glu	Lys	Gly	Thr	Phe	Pro	Phe	Ala	Leu	Glu	Ala	Glu	Thr	Val	Pro	805	810	815
Gln	Ala	Cys	Asp	Gly	Pro	Lys	Ala	His	Thr	Ser	Phe	Gln	Ile	Ser	Leu	820	825	830

Cura 468 SEQ list 0405.txt

Asn	Val	Ser	Tyr	Ile	Gly	Ser	Arg	Pro	Val	Ser	Asn	Met	Ala	Ile	Val
		835					840					845			
Asp	Val	Lys	Met	Val	Ser	Gly	Phe	Ile	Pro	Leu	Lys	Pro	Thr	Val	Lys
		850				855					860				
Asn	Leu	Glu	Lys	Ser	Glu	His	Ile	Ser	Arg	Thr	Glu	Val	Ser	Asn	Asn
865					870					875					880
His	Val	Leu	Ile	Tyr	Leu	Asp	Lys	Val	Ser	Asn	Gln	Thr	Leu	Ser	Leu
				885					890					895	
Ser	Phe	Phe	Val	Val	Gln	Asp	Ile	Glu	Val	Arg	Asp	Leu	Lys	Pro	Ala
			900					905					910		
Ile	Ile	Lys	Val	Tyr	Asp	Tyr	Tyr	Glu	Thr	Asn	Glu	Phe	Ala	Ile	Ala
		915					920					925			
Glu	Tyr	His	Ala	Pro	Cys	Ser	Lys	Asp	Pro	Gly	Asn	Ala			
	930					935					940				

<210> 40  
 <211> 373  
 <212> PRT  
 <213> Mus musculus

<400> 40

Met	Ser	Thr	Asp	Cys	Ala	Gly	Asn	Ser	Thr	Cys	Pro	Val	Asn	Ser	Thr
1				5					10					15	
Glu	Glu	Asp	Pro	Pro	Val	Gly	Met	Glu	Gly	His	Ala	Asn	Leu	Lys	Leu
			20					25					30		
Leu	Phe	Thr	Val	Leu	Ser	Ala	Val	Met	Val	Gly	Leu	Val	Met	Phe	Ser
		35					40					45			
Phe	Gly	Cys	Ser	Val	Glu	Ser	Gln	Lys	Leu	Trp	Leu	His	Leu	Arg	Arg
	50					55					60				
Pro	Trp	Gly	Ile	Ala	Val	Gly	Leu	Leu	Ser	Gln	Phe	Gly	Leu	Met	Pro
65					70					75					80
Leu	Thr	Ala	Tyr	Leu	Leu	Ala	Ile	Gly	Phe	Gly	Leu	Lys	Pro	Phe	Gln
				85				90						95	
Ala	Ile	Ala	Val	Leu	Met	Met	Gly	Ser	Cys	Pro	Gly	Gly	Thr	Ile	Ser
			100					105					110		

Cura 468 SEQ list 0405.txt

Asn	Val	Leu	Thr	Phe	Trp	Val	Asp	Gly	Asp	Met	Asp	Leu	Ser	Ile	Ser	
		115					120					125				
Met	Thr	Thr	Cys	Ser	Thr	Val	Ala	Ala	Leu	Gly	Met	Met	Pro	Leu	Cys	
	130					135					140					
Leu	Tyr	Ile	Tyr	Thr	Arg	Ser	Trp	Thr	Leu	Thr	Gln	Asn	Leu	Val	Ile	
145					150					155					160	
Pro	Tyr	Gln	Ser	Ile	Gly	Ile	Thr	Leu	Val	Ser	Leu	Val	Val	Pro	Val	
				165					170					175		
Ala	Ser	Gly	Val	Tyr	Val	Asn	Tyr	Arg	Trp	Pro	Lys	Gln	Ala	Thr	Val	
			180					185					190			
Ile	Leu	Lys	Val	Gly	Ala	Ile	Leu	Gly	Gly	Met	Leu	Leu	Leu	Val	Val	
		195					200					205				
Ala	Val	Thr	Gly	Met	Val	Leu	Ala	Lys	Gly	Trp	Asn	Thr	Asp	Val	Thr	
	210					215					220					
Leu	Leu	Val	Ile	Ser	Cys	Ile	Phe	Pro	Leu	Val	Gly	His	Val	Thr	Gly	
225					230					235					240	
Phe	Leu	Leu	Ala	Phe	Leu	Thr	His	Gln	Ser	Trp	Gln	Arg	Cys	Arg	Thr	
				245					250					255		
Ile	Ser	Ile	Glu	Thr	Gly	Ala	Gln	Asn	Ile	Gln	Leu	Cys	Ile	Ala	Met	
			260					265					270			
Leu	Gln	Leu	Ser	Phe	Ser	Ala	Glu	Tyr	Leu	Val	Gln	Leu	Leu	Asn	Phe	
		275					280					285				
Ala	Leu	Ala	Tyr	Gly	Leu	Phe	Gln	Val	Leu	His	Gly	Leu	Leu	Ile	Val	
	290					295					300					
Ala	Ala	Tyr	Gln	Ala	Tyr	Lys	Arg	Arg	Gln	Lys	Ser	Lys	Cys	Arg	Arg	
305					310					315					320	
Gln	His	Pro	Asp	Cys	Pro	Asp	Val	Cys	Tyr	Glu	Lys	Gln	Pro	Arg	Glu	
				325					330					335		
Thr	Ser	Ala	Phe	Leu	Asp	Lys	Gly	Asp	Glu	Ala	Ala	Val	Thr	Leu	Gly	
			340					345					350			
Pro	Val	Gln	Pro	Glu	Gln	His	His	Arg	Ala	Ala	Glu	Leu	Thr	Ser	His	
		355					360					365				

Cura 468 SEQ list 0405.txt

Ile Pro Ser Cys Glu  
370

<210> 41

<211> 347

<212> PRT

<213> Orycctolagus cuniculus

<400> 41

Met	Ser	Asn	Leu	Thr	Val	Gly	Cys	Leu	Ala	Asn	Ala	Thr	Val	Cys	Glu
1				5					10					15	

Gly	Ala	Ser	Cys	Val	Ala	Pro	Glu	Ser	Asn	Phe	Asn	Ala	Ile	Leu	Ser
			20					25					30		

Val	Val	Leu	Ser	Thr	Val	Leu	Thr	Ile	Leu	Leu	Ala	Leu	Val	Met	Phe
		35					40					45			

Ser	Met	Gly	Cys	Asn	Val	Glu	Ile	Lys	Lys	Phe	Leu	Gly	His	Ile	Arg
	50					55					60				

Arg	Pro	Trp	Gly	Ile	Phe	Ile	Gly	Phe	Leu	Cys	Gln	Phe	Gly	Ile	Met
65					70					75					80

Pro	Leu	Thr	Gly	Phe	Val	Leu	Ala	Val	Ala	Phe	Gly	Ile	Met	Pro	Ile
				85					90					95	

Gln	Ala	Val	Val	Val	Leu	Ile	Met	Gly	Cys	Cys	Pro	Gly	Gly	Thr	Ala
			100					105					110		

Ser	Asn	Ile	Leu	Ala	Tyr	Trp	Val	Asp	Gly	Asp	Met	Asp	Leu	Ser	Val
		115					120					125			

Ser	Met	Thr	Thr	Cys	Ser	Thr	Leu	Leu	Ala	Leu	Gly	Met	Met	Pro	Leu
	130					135					140				

Cys	Leu	Tyr	Val	Tyr	Thr	Lys	Met	Trp	Val	Asp	Ser	Gly	Thr	Ile	Val
145					150					155					160

Ile	Pro	Tyr	Asp	Asn	Ile	Gly	Thr	Ser	Leu	Val	Ala	Leu	Val	Val	Pro
				165					170					175	

Val	Ser	Ile	Gly	Met	Phe	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys
			180					185					190		

Ile	Ile	Leu	Lys	Val	Gly	Ser	Ile	Ala	Gly	Ala	Val	Leu	Ile	Val	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## Cura 468 SEQ list 0405.txt

195

200

205

Ile	Ala	Val	Val	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Glu
210						215					220				
Pro	Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Met	Ala	Gly	Tyr	Ser
225					230					235					240
Leu	Gly	Phe	Phe	Leu	Ala	Arg	Ile	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys
				245					250					255	
Arg	Thr	Val	Ala	Leu	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser
			260					265					270		
Thr	Ile	Val	Gln	Leu	Ser	Phe	Ser	Pro	Glu	Asp	Leu	Thr	Tyr	Val	Phe
		275					280					285			
Thr	Phe	Pro	Leu	Ile	Tyr	Ser	Ile	Phe	Gln	Ile	Ala	Phe	Ala	Ala	Ile
	290					295					300				
Phe	Leu	Gly	Ile	Tyr	Val	Ala	Tyr	Arg	Lys	Cys	His	Gly	Lys	Asn	Asp
305					310					315					320
Ala	Glu	Phe	Pro	Asp	Ile	Lys	Asp	Thr	Lys	Thr	Glu	Pro	Glu	Ser	Ser
				325					330					335	
Phe	His	Gln	Met	Asn	Gly	Gly	Phe	Gln	Pro	Glu					
			340					345							

&lt;210&gt; 42

&lt;211&gt; 348

&lt;212&gt; PRT

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 42

Met	Asp	Asn	Ser	Ser	Val	Cys	Ser	Pro	Asn	Ala	Thr	Phe	Cys	Glu	Gly
1				5					10					15	
Asp	Ser	Cys	Leu	Val	Thr	Glu	Ser	Asn	Phe	Asn	Ala	Ile	Leu	Ser	Thr
			20					25					30		
Val	Met	Ser	Thr	Val	Leu	Thr	Ile	Leu	Leu	Ala	Met	Val	Met	Phe	Ser
		35					40					45			
Met	Gly	Cys	Asn	Val	Glu	Ile	Asn	Lys	Phe	Leu	Gly	His	Ile	Lys	Arg
	50					55					60				

## Cura 468 SEQ list 0405.txt

Pro	Trp	Gly	Ile	Phe	Val	Gly	Phe	Leu	Cys	Gln	Phe	Gly	Ile	Met	Pro	65	70	75	80
Leu	Thr	Gly	Phe	Ile	Leu	Ser	Val	Ala	Ser	Gly	Ile	Leu	Pro	Val	Gln		85	90	95
Ala	Val	Val	Val	Leu	Ile	Met	Gly	Cys	Cys	Pro	Gly	Gly	Thr	Gly	Ser		100	105	110
Asn	Ile	Leu	Ala	Tyr	Trp	Ile	Asp	Gly	Asp	Met	Asp	Leu	Ser	Val	Ser		115	120	125
Met	Thr	Thr	Cys	Ser	Thr	Leu	Leu	Ala	Leu	Gly	Met	Met	Pro	Leu	Cys		130	135	140
Leu	Phe	Ile	Tyr	Thr	Lys	Met	Trp	Val	Asp	Ser	Gly	Thr	Ile	Val	Ile	145	150	155	160
Pro	Tyr	Asp	Ser	Ile	Gly	Ile	Ser	Leu	Val	Ala	Leu	Val	Ile	Pro	Val		165	170	175
Ser	Ile	Gly	Met	Phe	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys	Ile		180	185	190
Ile	Leu	Lys	Ile	Gly	Ser	Ile	Ala	Gly	Ala	Ile	Leu	Ile	Val	Leu	Ile		195	200	205
Ala	Val	Val	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Glu	Pro		210	215	220
Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Ile	Ala	Gly	Tyr	Ser	Leu	225	230	235	240
Gly	Phe	Phe	Leu	Ala	Arg	Leu	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys	Arg		245	250	255
Thr	Val	Ala	Leu	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser	Thr		260	265	270
Ile	Val	Gln	Leu	Ser	Phe	Ser	Pro	Glu	Asp	Leu	Asn	Leu	Val	Phe	Thr		275	280	285
Phe	Pro	Leu	Ile	Tyr	Thr	Val	Phe	Gln	Leu	Val	Phe	Ala	Ala	Ile	Ile		290	295	300
Leu	Gly	Met	Tyr	Val	Thr	Tyr	Lys	Lys	Cys	His	Gly	Lys	Asn	Asp	Ala	305	310	315	320

Cura 468 SEQ list 0405.txt

Glu Phe Leu Glu Lys Thr Asp Asn Asp Met Asp Pro Met Pro Ser Phe  
325 330 335

Gln Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys  
340 345

<210> 43

<211> 348

<212> PRT

<213> Mus musculus

<400> 43

Met Asp Asn Ser Ser Val Cys Pro Pro Asn Ala Thr Val Cys Glu Gly  
1 5 10 15

Asp Ser Cys Val Val Pro Glu Ser Asn Phe Asn Ala Ile Leu Asn Thr  
20 25 30

Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Met Val Met Phe Ser  
35 40 45

Met Gly Cys Asn Val Glu Val His Lys Phe Leu Gly His Ile Lys Arg  
50 55 60

Pro Trp Gly Ile Phe Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro  
65 70 75 80

Leu Thr Gly Phe Ile Leu Ser Val Ala Ser Gly Ile Leu Pro Val Gln  
85 90 95

Ala Val Val Val Leu Ile Met Gly Cys Cys Pro Gly Gly Thr Gly Ser  
100 105 110

Asn Ile Leu Ala Tyr Trp Ile Asp Gly Asp Met Asp Leu Ser Val Ser  
115 120 125

Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys  
130 135 140

Leu Phe Val Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile  
145 150 155 160

Pro Tyr Asp Ser Ile Gly Ile Ser Leu Val Ala Leu Val Ile Pro Val  
165 170 175

Ser Phe Gly Met Phe Val Asn His Lys Trp Pro Gln Lys Ala Lys Ile  
180 185 190

Cura 468 SEQ list 0405.txt

Ile	Leu	Lys	Ile	Gly	Ser	Ile	Thr	Gly	Val	Ile	Leu	Ile	Val	Leu	Ile
		195					200					205			
Ala	Val	Ile	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Glu	Pro
	210					215					220				
Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Ile	Ala	Gly	Tyr	Ser	Leu
225					230					235					240
Gly	Phe	Phe	Leu	Ala	Arg	Leu	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys	Arg
				245					250					255	
Thr	Val	Ala	Leu	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser	Thr
			260					265					270		
Ile	Val	Gln	Leu	Ser	Phe	Ser	Pro	Glu	Asp	Leu	Asn	Leu	Val	Phe	Thr
		275					280					285			
Phe	Pro	Leu	Ile	Tyr	Thr	Val	Phe	Gln	Leu	Val	Phe	Ala	Ala	Val	Ile
	290					295					300				
Leu	Gly	Ile	Tyr	Val	Thr	Tyr	Arg	Lys	Cys	Tyr	Gly	Lys	Asn	Asp	Ala
305					310					315					320
Glu	Phe	Leu	Glu	Lys	Thr	Asp	Asn	Glu	Met	Asp	Ser	Arg	Pro	Ser	Phe
				325					330					335	
Asp	Glu	Thr	Asn	Lys	Gly	Phe	Gln	Pro	Asp	Glu	Lys				
			340					345							

<210> 44  
 <211> 348  
 <212> PRT  
 <213> Mus musculus

<400> 44															
Met	Asp	Asn	Ser	Ser	Val	Cys	Pro	Pro	Asn	Ala	Thr	Val	Cys	Glu	Gly
1				5					10					15	
Asp	Ser	Cys	Val	Val	Pro	Glu	Ser	Asn	Phe	Asn	Ala	Ile	Leu	Asn	Thr
			20					25					30		
Val	Met	Ser	Thr	Val	Leu	Thr	Ile	Leu	Leu	Ala	Met	Val	Met	Phe	Ser
		35					40					45			
Met	Gly	Cys	Asn	Val	Glu	Val	His	Lys	Phe	Leu	Gly	His	Ile	Lys	Arg



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55

60

Pro	Trp	Gly	Ile	Phe	Val	Gly	Phe	Leu	Cys	Gln	Phe	Gly	Ile	Met	Pro
65					70					75					80
Leu	Thr	Gly	Phe	Ile	Leu	Ser	Val	Ala	Ser	Gly	Ile	Leu	Pro	Val	Gln
				85					90					95	
Ala	Val	Val	Val	Leu	Ile	Met	Gly	Cys	Cys	Pro	Gly	Gly	Thr	Gly	Ser
			100					105					110		
Asn	Ile	Leu	Ala	Tyr	Trp	Ile	Asp	Gly	Asp	Met	Asp	Leu	Ser	Val	Ser
		115					120					125			
Met	Thr	Thr	Cys	Ser	Thr	Leu	Leu	Ala	Leu	Gly	Met	Met	Pro	Leu	Cys
	130					135					140				
Leu	Phe	Val	Tyr	Thr	Lys	Met	Trp	Val	Asp	Ser	Gly	Thr	Ile	Val	Ile
145					150					155					160
Pro	Tyr	Asp	Ser	Ile	Gly	Ile	Ser	Leu	Val	Ala	Leu	Val	Ile	Pro	Val
				165					170					175	
Ser	Phe	Gly	Met	Phe	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys	Ile
			180					185					190		
Ile	Leu	Lys	Ile	Gly	Ser	Ile	Thr	Gly	Val	Ile	Leu	Ile	Val	Leu	Ile
		195					200					205			
Ala	Val	Ile	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Ile	Ile	Glu	Pro
	210					215					220				
Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Phe	Pro	Ile	Ala	Gly	Tyr	Ser	Leu
225					230					235					240
Gly	Phe	Phe	Leu	Ala	Arg	Leu	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys	Arg
				245					250					255	
Thr	Val	Ala	Leu	Glu	Thr	Gly	Met	Gln	Asn	Thr	Gln	Leu	Cys	Ser	Thr
			260					265					270		
Ile	Val	Gln	Leu	Ser	Phe	Ser	Pro	Glu	Asp	Leu	Asn	Leu	Val	Phe	Thr
		275					280					285			
Phe	Pro	Leu	Ile	Tyr	Thr	Val	Phe	Gln	Leu	Val	Phe	Ala	Ala	Val	Ile
	290					295					300				
Leu	Gly	Ile	Tyr	Val	Thr	Tyr	Arg	Lys	Cys	Tyr	Gly	Lys	Asn	Asp	Ala

305 310 315 320

Glu Phe Leu Glu Lys Thr Asp Asn Glu Met Asp Ser Arg Pro Ser Phe  
325 330 335

Asp Glu Thr Asn Lys Gly Phe Gln Pro Asp Glu Lys  
340 345

<210> 45

<211> 348

<212> PRT

<213> Homo sapiens

<400> 45

Met Asp Asn Ser Ser Ile Cys Asn Pro Asn Ala Thr Ile Cys Glu Gly  
1 5 10 15

Asp Ser Cys Ile Ala Pro Glu Ser Asn Phe Asn Ala Ile Leu Ser Val  
20 25 30

Val Met Ser Thr Val Leu Thr Ile Leu Leu Ala Leu Val Met Phe Ser  
35 40 45

Met Gly Cys Asn Val Glu Leu His Lys Phe Leu Gly His Leu Arg Arg  
50 55 60

Pro Trp Gly Ile Val Val Gly Phe Leu Cys Gln Phe Gly Ile Met Pro  
65 70 75 80

Leu Thr Gly Phe Val Leu Ser Val Ala Phe Gly Ile Leu Pro Val Gln  
85 90 95

Ala Val Val Val Leu Ile Gln Gly Cys Cys Pro Gly Gly Thr Ala Ser  
100 105 110

Asn Ile Leu Ala Tyr Trp Val Asp Gly Asp Met Asp Leu Ser Val Ser  
115 120 125

Met Thr Thr Cys Ser Thr Leu Leu Ala Leu Gly Met Met Pro Leu Cys  
130 135 140

Leu Phe Ile Tyr Thr Lys Met Trp Val Asp Ser Gly Thr Ile Val Ile  
145 150 155 160

Pro Tyr Asp Ser Ile Gly Thr Ser Leu Val Ala Leu Val Ile Pro Val  
165 170 175

Cura 468 SEQ list 0405.txt

Ser	Ile	Gly	Met	Tyr	Val	Asn	His	Lys	Trp	Pro	Gln	Lys	Ala	Lys	Ile
			180					185					190		
Ile	Leu	Lys	Ile	Gly	Ser	Ile	Ala	Gly	Ala	Ile	Leu	Ile	Val	Leu	Ile
		195					200					205			
Ala	Val	Val	Gly	Gly	Ile	Leu	Tyr	Gln	Ser	Ala	Trp	Thr	Ile	Glu	Pro
		210				215					220				
Lys	Leu	Trp	Ile	Ile	Gly	Thr	Ile	Tyr	Pro	Ile	Ala	Gly	Tyr	Gly	Leu
225					230					235					240
Gly	Phe	Phe	Leu	Ala	Arg	Ile	Ala	Gly	Gln	Pro	Trp	Tyr	Arg	Cys	Arg
				245					250					255	
Thr	Val	Ala	Leu	Glu	Thr	Gly	Leu	Gln	Asn	Thr	Gln	Leu	Cys	Ser	Thr
			260					265					270		
Ile	Val	Gln	Leu	Ser	Phe	Ser	Pro	Glu	Asp	Leu	Asn	Leu	Val	Phe	Thr
		275					280					285			
Phe	Pro	Leu	Ile	Tyr	Ser	Ile	Phe	Gln	Ile	Ala	Phe	Ala	Ala	Ile	Leu
		290				295					300				
Leu	Gly	Ala	Tyr	Val	Ala	Tyr	Lys	Lys	Cys	His	Gly	Lys	Asn	Asn	Thr
305					310					315					320
Glu	Leu	Gln	Glu	Lys	Thr	Asp	Asn	Glu	Met	Glu	Pro	Arg	Ser	Ser	Phe
				325					330					335	
Gln	Glu	Thr	Asn	Lys	Gly	Phe	Gln	Pro	Asp	Glu	Lys				
			340					345							

<210> 46  
 <211> 272  
 <212> PRT  
 <213> Homo sapiens

<400> 46

Met	Ala	Ala	Lys	Val	Phe	Glu	Ser	Ile	Gly	Lys	Phe	Gly	Leu	Ala	Leu
1				5					10					15	
Ala	Val	Ala	Gly	Gly	Val	Val	Asn	Ser	Ala	Leu	Tyr	Asn	Val	Asp	Ala
			20					25					30		
Gly	His	Arg	Ala	Val	Ile	Phe	Asp	Arg	Phe	Arg	Gly	Val	Gln	Asp	Ile
		35					40					45			

Cura 468 SEQ list 0405.txt

Val	Val	Gly	Glu	Gly	Thr	His	Phe	Leu	Ile	Pro	Trp	Val	Gln	Lys	Pro
	50					55					60				
Ile	Ile	Phe	Asp	Cys	Arg	Ser	Arg	Pro	Arg	Asn	Val	Pro	Val	Ile	Thr
65					70					75					80
Gly	Ser	Lys	Asp	Leu	Gln	Asn	Val	Asn	Ile	Thr	Leu	Arg	Ile	Leu	Phe
				85					90					95	
Arg	Pro	Val	Ala	Ser	Gln	Leu	Pro	Arg	Ile	Phe	Thr	Ser	Ile	Gly	Glu
			100					105					110		
Asp	Tyr	Asp	Glu	Arg	Val	Leu	Pro	Ser	Ile	Thr	Thr	Glu	Ile	Leu	Lys
		115					120					125			
Ser	Val	Val	Ala	Arg	Phe	Asp	Ala	Gly	Glu	Leu	Ile	Thr	Gln	Arg	Glu
	130					135					140				
Leu	Val	Ser	Arg	Gln	Val	Ser	Asp	Asp	Leu	Thr	Glu	Arg	Ala	Ala	Thr
145					150					155					160
Phe	Gly	Leu	Ile	Leu	Asp	Asp	Val	Ser	Leu	Thr	His	Leu	Thr	Phe	Gly
				165					170					175	
Lys	Glu	Phe	Thr	Glu	Ala	Val	Glu	Ala	Lys	Gln	Val	Ala	Gln	Gln	Glu
			180					185					190		
Ala	Glu	Arg	Ala	Arg	Phe	Val	Val	Glu	Lys	Ala	Glu	Gln	Gln	Lys	Lys
		195					200					205			
Ala	Ala	Ile	Ile	Ser	Ala	Glu	Gly	Asp	Ser	Lys	Ala	Ala	Glu	Leu	Ile
	210					215					220				
Ala	Asn	Ser	Leu	Ala	Thr	Ala	Gly	Asp	Gly	Leu	Ile	Glu	Leu	Arg	Lys
225					230					235					240
Leu	Glu	Ala	Ala	Glu	Asp	Ile	Ala	Tyr	Gln	Leu	Ser	Arg	Ser	Arg	Asn
				245					250					255	
Ile	Thr	Tyr	Leu	Pro	Ala	Gly	Gln	Ser	Val	Leu	Leu	Gln	Leu	Pro	Gln
			260					265					270		

Cura 468 SEQ list 0405.txt

<211> 272

<212> PRT

<213> Rattus norvegicus

<400> 47

Met Ala Ala Lys Val Phe Glu Ser Ile Gly Lys Phe Gly Leu Ala Leu  
1 5 10 15

Ala Val Ala Gly Gly Val Val Asn Ser Ala Leu Tyr Asn Val Asp Ala  
20 25 30

Gly His Arg Ala Val Ile Phe Asp Arg Phe Arg Gly Val Gln Asp Ile  
35 40 45

Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln Lys Pro  
50 55 60

Ile Ile Phe Asp Cys Arg Ser Arg Pro Arg Asn Val Pro Val Ile Thr  
65 70 75 80

Gly Ser Lys Asp Leu Gln Asn Val Asn Ile Thr Leu Arg Ile Leu Phe  
85 90 95

Arg Pro Val Ala Ser Gln Leu Pro Arg Ile Tyr Thr Ser Ile Gly Glu  
100 105 110

Asp Tyr Asp Glu Arg Val Leu Pro Ser Ile Thr Thr Glu Ile Leu Lys  
115 120 125

Ser Val Val Ala Arg Phe Asp Ala Gly Glu Leu Ile Thr Gln Arg Glu  
130 135 140

Leu Val Ser Arg Gln Val Ser Asp Asp Leu Thr Glu Arg Ala Ala Thr  
145 150 155 160

Phe Gly Leu Ile Leu Asp Asp Val Ser Leu Thr His Leu Thr Phe Gly  
165 170 175

Lys Glu Phe Thr Glu Ala Val Glu Ala Lys Gln Val Ala Gln Gln Glu  
180 185 190

Ala Glu Arg Ala Arg Phe Val Val Glu Lys Ala Glu Gln Gln Lys Lys  
195 200 205

Ala Ala Ile Ile Ser Ala Glu Gly Asp Ser Lys Ala Ala Glu Leu Ile  
210 215 220

Ala Asn Ser Leu Ala Thr Ala Gly Asp Gly Leu Ile Glu Leu Arg Lys

## Cura 468 SEQ list 0405.txt

225		230		235		240									
Leu	Glu	Ala	Ala	Glu	Asp	Ile	Ala	Tyr	Gln	Leu	Ser	Arg	Ser	Arg	Asn
				245					250					255	
Ile	Thr	Tyr	Leu	Pro	Ala	Gly	Gln	Ser	Val	Leu	Leu	Gln	Leu	Pro	Gln
			260					265					270		

&lt;210&gt; 48

&lt;211&gt; 1798

&lt;212&gt; PRT

&lt;213&gt; Drosophila melanogaster

&lt;400&gt; 48

Met	Glu	Met	Arg	Glu	Val	Leu	Ser	Arg	Glu	Gly	Arg	Glu	Ala	Lys	Asn
1				5					10					15	
Leu	Leu	Val	Tyr	Gln	Phe	Cys	Asp	Glu	Thr	Thr	Ser	Ser	Gly	Ala	Thr
			20					25					30		
Ser	Gly	Phe	Gly	Ser	Thr	Gly	Gly	Asp	Val	Gly	Gly	Gly	Ser	Gly	Gly
		35					40					45			
Asp	Gly	Pro	Ala	Val	Gly	Ser	Gly	Gly	Val	Leu	Leu	Asn	Gly	Asp	Cys
	50					55					60				
Tyr	Arg	Lys	Pro	Pro	Met	Val	Pro	Pro	Lys	Ser	Pro	Asn	Gly	Thr	Pro
65					70					75					80
Lys	Asn	Cys	Gln	Ser	Pro	Thr	Ser	Pro	Arg	Leu	Lys	Ser	Ser	Ala	Ser
				85					90					95	
Val	Gly	Cys	Gly	Gly	Gly	Ser	Ser	Gly	Gly	Pro	Arg	Val	Arg	Ser	Ala
			100					105					110		
Ser	Thr	Gly	Arg	Asp	Lys	Lys	Ser	Glu	Leu	Gln	Ala	Arg	Tyr	Trp	Ala
		115					120					125			
Leu	Leu	Phe	Gly	Asn	Leu	Gln	Arg	Ala	Ile	Asn	Glu	Ile	Tyr	Gln	Thr
	130					135					140				
Val	Glu	Cys	Tyr	Glu	Asn	Ile	Ser	Ser	Cys	Gln	Glu	Thr	Ile	Leu	Val
145					150					155					160

Cura 468 SEQ list 0405.txt

Leu	Glu	Asn	Tyr	Val	Arg	Asp	Phe	Lys	Ala	Leu	Cys	Glu	Trp	Phe	Lys	165	170	175
Val	Ser	Trp	Asp	Tyr	Glu	Ser	Arg	Pro	Leu	Gln	Gln	Arg	Pro	Gln	Ser	180	185	190
Leu	Ala	Trp	Glu	Val	Arg	Lys	Ser	Asn	Pro	Thr	Pro	Arg	Val	Arg	Thr	195	200	205
Arg	Ser	Leu	Cys	Ser	Pro	Asn	Asn	Ser	Gly	Lys	Ser	Ser	Pro	Ala	Leu	210	215	220
Phe	Pro	Gly	Thr	Gln	Ser	Gly	Glu	Thr	Ser	Pro	Phe	Cys	Asp	Asn	Gly	225	230	235
Gln	Ile	Ser	Pro	Arg	Lys	Leu	Leu	Arg	Ala	Tyr	Asp	Gln	Val	Pro	Lys	245	250	255
Gly	Ala	Met	Arg	Leu	Asn	Val	Arg	Glu	Leu	Phe	Ala	Ala	Ser	Lys	Arg	260	265	270
Ala	Thr	Gln	Gly	Ser	Ser	Gln	Ser	Asp	Asn	Met	Glu	Gly	Pro	Leu	Asp	275	280	285
Leu	Ser	Gly	Asp	Lys	Ser	Asn	Phe	Val	Leu	Arg	Ser	Thr	Gln	Tyr	Ala	290	295	300
Gln	Thr	Asp	Leu	Glu	Asp	Pro	His	Leu	Thr	Leu	Ala	Asp	Val	Arg	Glu	305	310	315
Lys	Met	Arg	Met	Glu	Ala	Glu	Glu	Arg	Glu	Ala	Gln	Asn	Arg	Ile	Glu	325	330	335
Asn	Glu	Ala	Leu	Glu	Glu	Val	Thr	Ile	Pro	Ile	Asp	Asn	Glu	Asp	Ala	340	345	350
Thr	Glu	Ser	Leu	Asn	Lys	Gln	Glu	Pro	Ser	Ser	Leu	Glu	Leu	Pro	Ile	355	360	365
His	Asn	Val	Ala	Asp	Leu	Ser	Lys	Glu	Pro	Glu	Leu	Met	Glu	Ala	Ala	370	375	380
Ser	Glu	Ala	Thr	Ala	Leu	Glu	Met	Thr	Val	Ala	Ser	Leu	Glu	Ser	Met	385	390	395
Glu	Asn	Ala	Leu	Leu	Asn	Gln	Gln	Ala	Asn	Lys	Glu	Pro	Thr	Pro	Pro	405	410	415

## Cura 468 SEQ list 0405.txt

Ser	Thr	Val	Ile	Lys	Pro	Leu	Ala	Glu	Ile	Leu	Lys	Lys	Pro	Gln	Pro	420	425	430
Leu	Asn	Pro	Leu	Ser	Gly	Asn	Asn	Val	Gln	Asn	Ser	Pro	Leu	Lys	Tyr	435	440	445
Ser	Ser	Val	Leu	Asn	Arg	Pro	Ser	Lys	Lys	Met	Ile	Pro	Pro	Pro	Gly	450	455	460
Gly	Val	Ala	Ala	Gln	Lys	Thr	Ile	Ser	Thr	Lys	Pro	Gly	Leu	Val	Lys	465	470	475
Pro	Asn	Leu	Thr	Thr	Thr	Val	Asn	Gly	Leu	Arg	Ser	Thr	Lys	Thr	Ala	485	490	495
Thr	Ala	Pro	Pro	Ala	Ile	Lys	Thr	Thr	Gly	Arg	Ser	Gly	Leu	Gln	Arg	500	505	510
His	Pro	Arg	Pro	Ser	Ser	Lys	Thr	Glu	Cys	Tyr	Gly	Pro	Pro	Asn	Asn	515	520	525
Val	Ala	Ser	Arg	Leu	Ser	Ala	Arg	Ser	Arg	Thr	Ile	Asn	Thr	Leu	Lys	530	535	540
Ala	Glu	Asn	Gln	His	Ser	Glu	Pro	Lys	Gln	Ile	Gln	Pro	Pro	Thr	Asp	545	550	555
Ala	Asp	Asp	Gly	Trp	Leu	Thr	Val	Lys	Asn	Arg	Arg	Arg	Thr	Ser	Met	565	570	575
His	Trp	Ala	Asn	Arg	Phe	Asn	Gln	Pro	Thr	Gly	Tyr	Ala	Ser	Leu	Pro	580	585	590
Thr	Leu	Ala	Leu	Leu	Asn	Glu	Gln	Gln	Lys	Glu	Gln	Glu	His	Lys	Glu	595	600	605
Lys	Gln	Lys	Gly	Glu	Asp	Asp	Gly	Lys	Val	Ile	Val	Lys	Thr	Ile	Ser	610	615	620
Ala	Lys	Thr	Lys	Ala	Pro	Ile	Glu	Val	Ala	Lys	Ala	Lys	Ala	Lys	Thr	625	630	635
Ser	Ile	Val	Ile	Thr	Arg	Pro	Glu	Ile	Lys	Asn	Ala	Lys	Ala	Lys	Val	645	650	655
Asn	Ser	Phe	Pro	Val	Gln	Lys	Ser	Asn	Thr	Asn	Gln	Val	Lys	Lys	Pro	660	665	670



Cura 468 SEQ list 0405.txt

Glu	Lys	Gln	Glu	Lys	Ser	Asp	Thr	Thr	Ala	Pro	Ala	Ala	Ile	Ala	Ser	675	680	685	
Ser	Arg	Leu	Lys	Met	Thr	Ser	Leu	His	Lys	Glu	Tyr	Met	Arg	Ser	Glu	690	695	700	
Lys	Asn	Ala	Leu	Arg	Lys	Leu	Gln	Gln	Lys	Glu	Gln	Gly	Asn	Gln	Gln	705	710	715	720
His	Asn	Ser	Ser	Ser	Ser	Ser	Ala	Glu	Thr	Val	Val	Glu	Ser	Cys	Asn	725	730	735	
Glu	Asp	His	Ser	Lys	Ile	Asp	Ile	Lys	Ile	Gln	Thr	Asn	Cys	Glu	Phe	740	745	750	
Ser	Lys	Thr	Ile	Gly	Glu	Leu	Tyr	Glu	Ser	Ile	Ala	His	Cys	Lys	Leu	755	760	765	
Pro	Ser	Gly	Ser	Leu	Lys	Thr	Asn	Ala	Ser	Thr	Leu	Ser	Ala	Cys	Asp	770	775	780	
Glu	Asn	Glu	Glu	Gln	Asn	Thr	Asp	Asp	Asn	Glu	Glu	Glu	Arg	Asn	Glu	785	790	795	800
Arg	Ile	Leu	Gly	Glu	Val	Gln	Glu	Ser	Leu	Glu	Arg	Gln	Ile	Arg	Glu	805	810	815	
Leu	Glu	Gln	Thr	Glu	Ile	Asp	Val	Asp	Thr	Glu	Thr	Asp	Glu	Thr	Asp	820	825	830	
Cys	Glu	Val	Gln	Leu	Glu	Glu	Gln	Asp	Asp	Gly	Val	Asp	Gly	Leu	Glu	835	840	845	
Met	Gly	Ser	Gly	Asp	Asp	Ser	Ala	Val	Phe	Val	Thr	Met	Ser	Asp	Asp	850	855	860	
Glu	Asn	Ala	Ser	Leu	Glu	Leu	Arg	Tyr	Gln	Ala	Leu	Leu	Ser	Asp	Met	865	870	875	880
Ser	Trp	Asn	Glu	Arg	Ala	Glu	Ala	Leu	Ala	Thr	Leu	Gln	Ala	Tyr	Val	885	890	895	
Ala	Arg	His	Pro	Gly	Arg	Ala	Gln	Glu	Leu	His	Gln	Lys	Leu	Ser	Ser	900	905	910	
Pro	Ser	Arg	Arg	Arg	Ser	Leu	Gln	Glu	Thr	Leu	Lys	Lys	Tyr	Gln	Ala	915	920	925	

Cura 468 SEQ list 0405.txt

Lys	Gln	Ala	Arg	Ala	Gln	Gln	Lys	Arg	Asn	Leu	Leu	Gln	Gln	Glu	Lys	930	935	940
Ala	Ala	Lys	Leu	Gln	Gln	Leu	Phe	Ser	Arg	Val	Glu	Asp	Val	Lys	Ala	945	950	955
Ala	Lys	Asn	Gln	Ile	Ile	Glu	Asp	Lys	Arg	Gln	Lys	Met	Gln	Gly	Arg	965	970	975
Leu	Gln	Arg	Ala	Ala	Glu	Asn	Arg	Glu	Gln	Tyr	Leu	Lys	Gln	Ile	Ile	980	985	990
Glu	Lys	Ala	His	Asp	Glu	Glu	Lys	Lys	Leu	Lys	Glu	Ile	Asn	Phe	Ile	995	1000	1005
Lys	Asn	Ile	Glu	Ala	Gln	Asn	Lys	Arg	Leu	Asp	Leu	Leu	Glu	Ser	Ser	1010	1015	1020
Lys	Glu	Thr	Glu	Gly	Arg	Leu	Gln	Asp	Leu	Glu	Gln	Glu	Arg	Gln	Lys	1025	1030	1035
Arg	Val	Glu	Glu	Lys	Leu	Ala	Lys	Glu	Ala	Ala	Val	Glu	Arg	Arg	Arg	1045	1050	1055
Gln	Ala	Leu	Glu	Lys	Glu	Arg	Leu	Leu	Lys	Leu	Glu	Lys	Met	Asn	Glu	1060	1065	1070
Thr	Arg	Leu	Glu	Lys	Glu	Gln	Arg	Ile	Gly	Lys	Met	Gln	Glu	Gln	Lys	1075	1080	1085
Glu	Lys	Gln	Arg	Gln	Ala	Leu	Ala	Arg	Glu	Lys	Ala	Arg	Asp	Arg	Glu	1090	1095	1100
Glu	Arg	Leu	Leu	Ala	Leu	Gln	Val	Gln	Gln	Gln	Gln	Thr	Thr	Glu	Glu	1105	1110	1115
Leu	Gln	Arg	Lys	Ile	Leu	Gln	Lys	Gln	Met	Glu	Ser	Ala	Arg	Arg	His	1125	1130	1135
Glu	Glu	Asn	Ile	Glu	His	Ile	Arg	Gln	Arg	Ala	Leu	Glu	Leu	Thr	Ile	1140	1145	1150
Pro	Thr	Arg	Gln	Ala	Asp	Glu	Gly	Arg	Gly	Asp	Gln	Asp	Val	Ser	Glu	1155	1160	1165
Asp	Ile	Leu	Asn	Gly	Asn	Ala	Thr	Ser	Thr	Thr	Asn	Glu	Asp	Cys	Asp	1170	1175	1180

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Leu	Ser	Ser	Ser	Leu	Ser	Glu	Val	Gly	Gly	Asn	Asn	Ala	His	Thr	Arg	1185	1190	1195	1200
Ser	Tyr	Lys	Lys	Lys	Met	Lys	Lys	Leu	Lys	Gln	Arg	Met	Asn	Gln	Cys	1205	1210	1215	
Ala	Ala	Glu	Tyr	Leu	Glu	Ser	Leu	Glu	Ala	Leu	Pro	Ala	His	Ala	Arg	1220	1225	1230	
Arg	Asp	Ser	Thr	Val	Pro	Lys	Leu	Leu	Asn	Leu	Val	Val	Lys	Gly	Gly	1235	1240	1245	
Gly	Ala	Gln	Gly	Leu	Asp	Arg	Asn	Leu	Gly	Asn	Leu	Leu	Arg	Val	Ile	1250	1255	1260	
Pro	Lys	Ala	Gln	Thr	Leu	Asp	Phe	Leu	Ala	Phe	Leu	Cys	Met	Asp	Gly	1265	1270	1275	1280
Leu	Gly	Ile	Leu	Ala	Asn	His	Val	Ile	Ser	Lys	Gly	Met	Asp	Glu	Asn	1285	1290	1295	
Ser	Glu	Ile	Ser	Arg	Lys	Ser	Val	Tyr	Leu	Ala	Ala	Gln	Leu	Tyr	Arg	1300	1305	1310	
Asn	Ala	Cys	Ser	Val	Cys	Pro	Gln	Ile	Ala	Arg	His	Ala	Leu	Leu	Gly	1315	1320	1325	
Asn	Ser	Ile	Thr	Val	Leu	Phe	Asp	Ala	Ile	Asn	Lys	Ser	Phe	Gln	Val	1330	1335	1340	
Ile	Leu	Lys	Ser	Asn	Arg	Cys	Thr	Lys	Glu	Thr	Phe	Ser	Asn	Phe	Trp	1345	1350	1355	1360
Pro	Pro	Lys	Met	Leu	His	Asn	Lys	Ser	Val	Ala	Arg	Gln	Ser	Ser	Arg	1365	1370	1375	
Leu	Glu	Ala	Leu	Ser	Leu	Pro	Glu	Glu	Lys	Ser	Pro	Gln	His	Pro	Val	1380	1385	1390	
Glu	Leu	Ser	Thr	Glu	Leu	Met	Leu	Ala	Cys	Thr	Glu	Ala	Leu	Ser	Ser	1395	1400	1405	
Ser	Tyr	Val	Lys	Lys	Asn	Thr	His	Pro	Lys	Val	Pro	Glu	Arg	Leu	Pro	1410	1415	1420	
Asp	Met	Ile	Asn	Asp	Cys	Arg	Phe	His	Trp	Gln	Asp	Val	Asn	Lys	Glu	1425	1430	1435	1440

Cura 468 SEQ list 0405.txt

Asp Met Leu Ala Asp	Glu Phe Arg Lys Tyr	Lys Cys Tyr Glu Lys Asn
1445	1450	1455
Pro Val Ile Ala Leu	Pro His Pro Ser Leu	Ser Ala Ser Leu Cys Arg
1460	1465	1470
Ser Leu Ser Ala Thr	Pro Leu Lys Ile Asn	Leu His Gln Phe Leu Gly
1475	1480	1485
Ser Gly Ile Leu Ile	Leu Arg Leu Asn His	His Arg His Pro Ala Thr
1490	1495	1500
Gly Ala Ser Phe Ser	Asp Ser Cys Cys Thr	Cys Cys Pro Lys Leu Thr
1505	1510	1515
Thr Glu Ala Ala Val	Ala Ala Val Ala Ala	His Gln His Gln His Gln
1525	1530	1535
Asn Gln Gln Gln Gln	Pro Asp Tyr Ala Val	Ile Thr Gly Leu Ile Glu
1540	1545	1550
Ile Leu Ser Arg Arg	Ile Gln Lys Val Arg	Glu Ser Ile Glu Ser Asn
1555	1560	1565
Lys Ser Val Met Leu	Ser Leu Leu Thr Thr	Leu Gly Phe Leu Ser Arg
1570	1575	1580
Phe Ile Asp Val Cys	Gln Pro Gly Pro Ala	Asp Pro Thr Arg Leu Leu
1585	1590	1595
Ser Ala Ala Lys Ser	Thr Glu Leu Phe Gly	Thr Val Ser Met Leu Tyr
1605	1610	1615
Gly Cys Val Met Pro	Met Gly Glu Cys Ile	Pro Pro Arg Thr Thr Ala
1620	1625	1630
Leu Ala Ala Ser Thr	Phe His Leu Tyr Val	Ser Leu Ala Ser Leu Asp
1635	1640	1645
Val Asn Thr Phe Gln	Glu Thr Leu Thr Val	Glu Gly Pro Leu Ser Leu
1650	1655	1660
Lys Leu Leu Asp Val	Met Thr Val Ile Leu	Asn Cys Ser Leu Val Asn
1665	1670	1675
Asp Gln Trp Thr Thr	Asn Ser Glu Ser Cys	Pro Met Leu Ile Asp Leu
1685	1690	1695

Cura 468 SEQ list 0405.txt

Val Ala Ser Met Ala Phe Phe Cys Val Asn Asn Arg Arg His Gln Asp  
1700 1705 1710

Leu Leu Ile Ser Glu Gln Tyr Ala Val Ile Phe Lys Arg Met Ala Lys  
1715 1720 1725

Leu Pro Thr Gln Phe Asn Pro Val Ile Tyr Pro Phe Leu Val Thr Val  
1730 1735 1740

Ser Phe Asn Asn Pro Pro Ala Arg Glu Phe Leu Ser Lys Asp Phe Asp  
1745 1750 1755 1760

Leu Thr Phe Leu Asp Glu Tyr Ser Lys Ser Glu Met Ala Gln Arg Asn  
1765 1770 1775

Val Val Ile Lys Leu Ile Asn Ser Arg Thr Lys Asp Lys Ile Ser Ala  
1780 1785 1790

Gly Asn Lys Lys Asn Ala  
1795

<210> 49

<211> 274

<212> PRT

<213> Toxocara canis

<400> 49

Met Ala Gly Ala Gln Lys Leu Leu Gly Arg Leu Gly Gln Ile Gly Val  
1 5 10 15

Ala Leu Ala Val Thr Gly Gly Val Val Gln Ser Ala Leu Tyr Asn Val  
20 25 30

Asp Gly Gly Gln Arg Ala Val Ile Phe Asp Arg Phe Thr Gly Val Lys  
35 40 45

Pro Asp Val Val Gly Glu Gly Thr His Phe Leu Ile Pro Trp Val Gln  
50 55 60

Arg Pro Ile Ile Phe Asp Ile Arg Ser Thr Pro Arg Ala Ile Ser Thr  
65 70 75 80

Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Ser Ile Thr Leu Arg Ile  
85 90 95

Leu His Arg Pro Glu Pro Ser Lys Leu Pro Asn Ile Tyr Leu Asn Ile  
100 105 110

Cura 468 SEQ list 0405.txt

Gly	Gln	Asp	Tyr	Ala	Glu	Arg	Val	Leu	Pro	Ser	Ile	Thr	Asn	Glu	Val
		115					120					125			
Leu	Lys	Ala	Val	Val	Ala	Gln	Phe	Asp	Ala	His	Glu	Met	Ile	Thr	Gln
	130					135					140				
Arg	Glu	Ser	Val	Ser	His	Arg	Val	Ser	Val	Glu	Leu	Ser	Glu	Arg	Ala
145					150					155					160
Arg	Gln	Phe	Gly	Ile	Leu	Leu	Asp	Asp	Ile	Ala	Ile	Thr	His	Leu	Ser
				165					170					175	
Phe	Gly	Arg	Glu	Phe	Thr	Glu	Ala	Val	Glu	Met	Lys	Gln	Val	Ala	Gln
			180					185					190		
Gln	Glu	Ala	Glu	Lys	Ala	Arg	Tyr	Leu	Val	Glu	Thr	Ala	Glu	Gln	Met
		195					200					205			
Lys	Ile	Ala	Ala	Ile	Thr	Thr	Ala	Glu	Gly	Asp	Ala	Gln	Ala	Ala	Lys
	210					215					220				
Leu	Leu	Ala	Gln	Ala	Phe	Lys	Asp	Ala	Gly	Asp	Gly	Leu	Ile	Glu	Leu
225					230					235					240
Arg	Lys	Ile	Glu	Ala	Ala	Glu	Glu	Ile	Ala	Glu	Arg	Met	Ser	Lys	Thr
				245					250					255	
Arg	Asn	Val	Ile	Tyr	Leu	Pro	Gly	Asn	Gln	Asn	Thr	Leu	Phe	Asn	Leu
			260					265					270		

Pro Ala

<210> 50

<211> 402

<212> PRT

<213> Caenorhabditis elegans

<400> 50

Met	Glu	Lys	Tyr	Lys	Asn	Glu	Leu	Glu	Ile	Phe	Lys	Arg	Met	Tyr	Phe
1				5					10					15	

Lys	Asn	Tyr	Pro	Thr	Ser	Ser	Lys	Asp	Glu	Glu	Ala	Ala	Ala	Val	Ile
			20					25					30		

Gln	Lys	Gly	Gly	Glu	Phe	Ile	Gln	Glu	Ile	Leu	Pro	Thr	Ile	Ile	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

## Cura 468 SEQ list 0405.txt

35

40

45

Thr	Ser	Arg	Ala	Tyr	Asp	Thr	Asn	Gln	Lys	Ala	Leu	Leu	Leu	Ala	Glu
	50					55					60				
Gly	Gly	Lys	Met	Tyr	Asn	Val	Leu	Glu	Asp	Tyr	Asn	Glu	Thr	Ala	Glu
65					70					75					80
Lys	Met	Leu	Ser	Lys	Ser	Val	Arg	Met	Asn	Pro	Lys	Asn	Ala	Asp	Ala
				85					90					95	
Trp	His	Glu	Leu	Gly	Leu	Cys	Val	Met	Lys	Arg	Arg	Asp	Leu	Glu	Phe
			100					105					110		
Ala	Gln	Ser	Cys	Phe	Lys	Ile	Ala	Leu	Gly	Ile	Ser	Lys	Thr	Ala	Pro
		115					120					125			
Ile	Leu	Thr	Ser	Leu	Ala	Val	Ala	Met	Arg	Leu	Val	Ala	Leu	Glu	His
	130					135					140				
Pro	Glu	Pro	Ala	Gln	Ala	Glu	Ile	Arg	Thr	Lys	Ala	Met	Glu	Leu	Ile
145					150					155					160
Ile	Glu	Ala	Arg	Arg	Leu	Asp	Ser	Ala	Tyr	Gly	Pro	Ala	Asn	Ile	Ala
				165					170					175	
Phe	Ala	Thr	Gly	Leu	Phe	Tyr	Cys	Phe	Phe	Ser	Thr	Ala	Lys	Val	Glu
			180					185					190		
Leu	Lys	Phe	Leu	Asp	Lys	Val	Ile	Glu	Asn	Tyr	Lys	Lys	Ala	Leu	Glu
		195					200					205			
Cys	Glu	Leu	Ser	Arg	Thr	Asp	Pro	Gln	Val	Tyr	Ile	Asn	Met	Ala	Thr
	210					215					220				
Cys	Leu	Lys	Phe	Met	Glu	Lys	Tyr	Asp	Glu	Ala	Leu	Ala	Val	Leu	Gln
225					230					235					240
Lys	Ala	Val	Glu	Tyr	Asp	Pro	Arg	Asn	Glu	Leu	Glu	Thr	Arg	Glu	Lys
				245					250					255	
Leu	Ala	Ser	Phe	Val	Ser	Tyr	Leu	Ser	Lys	Phe	Thr	Asp	Ala	Ile	Gln
			260					265					270		
Lys	Lys	Gly	Lys	Met	Lys	Ala	Lys	Arg	Met	Gln	Glu	Met	Ile	Asn	Glu
		275					280					285			
Leu	Lys	Lys	Ser	Ser	Asp	Gly	Phe	Arg	Ala	Lys	Ile	Ile	Gly	Asn	Ile

## Cura 468 SEQ list 0405.txt

290

295

300

Gly His Asp Glu Thr Ile Pro Val Ala Leu Val Gly Val Asp Ala Ala  
305 310 315 320

Gly Glu Val Tyr Gly Ile Thr Ile Tyr Asn Cys Leu Ser Asn Phe Gly  
325 330 335

Phe Val Ile Gly Asp Thr Val Thr Ile Ala Lys Pro Asp Phe Arg Glu  
340 345 350

Ile Lys Asn Leu Thr Ile Pro Ser Asp Pro Glu Ile His Val Asp Ser  
355 360 365

Val Lys Trp Ile Arg Val Ala Thr Pro Thr Gln Met Lys Lys Asn Gly  
370 375 380

Val Pro Leu Pro Glu Ser Val Leu Ala Arg Ala Val Ala Ser Thr Gln  
385 390 395 400

Thr Lys

<210> 51

<211> 711

<212> PRT

<213> Homo sapiens

<400> 51

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Cys Leu Gly Val  
1 5 10 15

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr  
20 25 30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu  
35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met  
50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu  
65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly  
85 90 95



## Cura 468 SEQ list 0405.txt

Arg	Cys	Asp	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met
			100					105					110		
Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Thr	Val	Gly	Gly
		115					120					125			
Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr
	130					135					140				
Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro
145					150					155					160
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val
				165					170					175	
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val
			180					185					190		
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser
		195					200					205			
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro
	210					215					220				
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys
225					230					235					240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro
				245					250					255	
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala
			260					265					270		
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly
		275					280					285			
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys
	290					295					300				
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu
305					310					315					320
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp
				325					330					335	
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala
			340					345					350		

## Cura 468 SEQ list 0405.txt

Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln	
		355					360					365				
Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys	
	370					375					380					
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His	
385					390					395					400	
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu	
				405					410					415		
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	
			420					425					430			
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys	
		435					440					445				
Ala	Asp	Asp	Gln	Pro	Pro	Ser	Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Gln	
	450					455					460					
Phe	Glu	Lys	Cys	Gly	Lys	Arg	Val	Asp	Arg	Leu	Asp	Gln	Arg	Arg	Ser	
465					470					475					480	
Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	Ser	Pro	Trp	Thr	Val	
				485					490					495		
Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	Val	
			500					505					510			
Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys	His	
		515					520					525				
Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln	Asn	
	530					535					540					
Pro	Gln	His	Gly	Glu	Pro	Ser	Leu	Gln	Arg	Val	Pro	Val	Ala	Lys	Met	
545					550					555					560	
Val	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	Leu	Leu	Lys	Leu	Glu	Arg	
				565					570					575		
Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu	Ile	Cys	Leu	Pro	Pro	Glu	
			580					585					590			
Trp	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu	Ile	Ala	Gly	Trp	Gly	
		595					600					605				

Cura 468 SEQ list 0405.txt

Glu	Thr	Lys	Gly	Thr	Gly	Asn	Asp	Thr	Val	Leu	Asn	Val	Ala	Leu	Leu
610						615					620				
Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Ile	Lys	His	Arg	Gly	Arg	Val
625					630					635					640
Arg	Glu	Ser	Glu	Met	Cys	Thr	Glu	Gly	Leu	Leu	Ala	Pro	Val	Gly	Ala
				645					650					655	
Cys	Glu	Gly	Asp	Tyr	Gly	Gly	Pro	Leu	Ala	Cys	Phe	Thr	His	Asn	Cys
			660					665					670		
Trp	Val	Leu	Glu	Gly	Ile	Ile	Ile	Pro	Asn	Arg	Val	Cys	Ala	Arg	Ser
	675						680					685			
Arg	Trp	Pro	Ala	Val	Phe	Thr	Arg	Val	Ser	Val	Phe	Val	Asp	Trp	Ile
	690					695					700				
His	Lys	Val	Met	Arg	Leu	Gly									
705					710										

<210> 52  
 <211> 711  
 <212> PRT  
 <213> Homo sapiens

<400> 52															
Met	Gly	Trp	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Thr	Gln	Cys	Leu	Gly	Val
1				5					10					15	
Pro	Gly	Gln	Arg	Ser	Pro	Leu	Asn	Asp	Phe	Gln	Val	Leu	Arg	Gly	Thr
			20					25					30		
Glu	Leu	Gln	His	Leu	Leu	His	Ala	Val	Val	Pro	Gly	Pro	Trp	Gln	Glu
		35					40					45			
Asp	Val	Ala	Asp	Ala	Glu	Glu	Cys	Ala	Gly	Arg	Cys	Gly	Pro	Leu	Met
	50					55					60				
Asp	Cys	Arg	Ala	Phe	His	Tyr	Asn	Val	Ser	Ser	His	Gly	Cys	Gln	Leu
65					70					75					80
Leu	Pro	Trp	Thr	Gln	His	Ser	Pro	His	Thr	Arg	Leu	Arg	Arg	Ser	Gly
				85					90					95	
Arg	Cys	Asp	Leu	Phe	Gln	Lys	Lys	Asp	Tyr	Val	Arg	Thr	Cys	Ile	Met
			100					105					110		

Cura 468 SEQ list 0405.txt

Asn	Asn	Gly	Val	Gly	Tyr	Arg	Gly	Thr	Met	Ala	Thr	Thr	Val	Gly	Gly
		115					120					125			
Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr
	130					135					140				
Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro
145					150					155					160
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val
				165					170					175	
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val
			180					185					190		
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser
		195					200					205			
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro
	210					215					220				
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys
225					230					235					240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro
				245					250					255	
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala
			260					265					270		
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly
		275					280					285			
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys
	290					295					300				
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu
305					310					315					320
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp
				325					330					335	
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala
			340					345					350		
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln
		355					360					365			

Cura 468 SEQ list 0405.txt

Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys
	370					375					380				
Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Trp	Ser	Ala	Glu	Thr	Pro	His
385					390					395					400
Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu	Glu
				405					410					415	
Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr
			420					425					430		
Thr	Met	Asp	Pro	Arg	Thr	Pro	Phe	Asp	Tyr	Cys	Ala	Leu	Arg	Arg	Cys
		435					440					445			
Ala	Asp	Asp	Gln	Pro	Pro	Ser	Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Gln
	450					455					460				
Phe	Glu	Lys	Cys	Gly	Lys	Arg	Val	Asp	Arg	Leu	Asp	Gln	Arg	Arg	Ser
465					470					475					480
Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	Ser	Pro	Trp	Thr	Val
				485					490					495	
Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	Val
			500					505					510		
Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys	His
		515					520					525			
Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln	Asn
	530					535					540				
Pro	Gln	His	Gly	Glu	Pro	Ser	Leu	Gln	Arg	Val	Pro	Val	Ala	Lys	Met
545					550					555					560
Val	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	Leu	Leu	Lys	Leu	Glu	Arg
				565					570					575	
Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu	Ile	Cys	Leu	Pro	Pro	Glu
			580					585					590		
Trp	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu	Ile	Ala	Gly	Trp	Gly
		595					600					605			
Glu	Thr	Lys	Gly	Thr	Gly	Asn	Asp	Thr	Val	Leu	Asn	Val	Ala	Phe	Leu
	610					615					620				

Cura 468 SEQ list 0405.txt

Asn Val Ile Ser Asn Gln Glu Cys Asn Ile Lys His Arg Gly Arg Val  
625 630 635 640

Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala  
645 650 655

Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys  
660 665 670

Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser  
675 680 685

Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile  
690 695 700

His Lys Val Met Arg Leu Gly  
705 710

<210> 53

<211> 711

<212> PRT

<213> Homo sapiens

<400> 53

Met Gly Trp Leu Pro Leu Leu Leu Leu Leu Thr Gln Tyr Leu Gly Val  
1 5 10 15

Pro Gly Gln Arg Ser Pro Leu Asn Asp Phe Gln Val Leu Arg Gly Thr  
20 25 30

Glu Leu Gln His Leu Leu His Ala Val Val Pro Gly Pro Trp Gln Glu  
35 40 45

Asp Val Ala Asp Ala Glu Glu Cys Ala Gly Arg Cys Gly Pro Leu Met  
50 55 60

Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln Leu  
65 70 75 80

Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg Arg Ser Gly  
85 90 95

Arg Cys Asp Leu Phe Gln Lys Lys Asp Tyr Val Arg Thr Cys Ile Met  
100 105 110

Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly Gly

## Cura 468 SEQ list 0405.txt

115			120			125									
Leu	Pro	Cys	Gln	Ala	Trp	Ser	His	Lys	Phe	Pro	Asn	Asp	His	Lys	Tyr
	130					135					140				
Thr	Pro	Thr	Leu	Arg	Asn	Gly	Leu	Glu	Glu	Asn	Phe	Cys	Arg	Asn	Pro
145					150					155					160
Asp	Gly	Asp	Pro	Gly	Gly	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro	Ala	Val
				165					170					175	
Arg	Phe	Gln	Ser	Cys	Gly	Ile	Lys	Ser	Cys	Arg	Glu	Ala	Ala	Cys	Val
			180					185					190		
Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu	Ser
		195					200					205			
Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His	Pro
	210					215					220				
Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr	Cys
225					230					235					240
Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp	Pro
				245					250					255	
Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu	Ala
			260					265					270		
Gln	Pro	Arg	Gln	Glu	Ala	Thr	Thr	Val	Ser	Cys	Phe	Arg	Gly	Lys	Gly
		275					280					285			
Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro	Cys
	290					295					300				
Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro	Glu
305					310					315					320
Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp
				325					330					335	
Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg	Ala
			340					345					350		
Ala	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro	Gln
		355					360					365			
Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser	Lys

## Cura 468 SEQ list 0405.txt

370

375

380

Thr 385	Arg	Lys	Gly	Val	Gln 390	Cys	Gln	Arg	Trp	Ser 395	Ala	Glu	Thr	Pro	His 400
Lys	Pro	Gln	Phe	Thr 405	Phe	Thr	Ser	Glu	Pro 410	His	Ala	Gln	Leu	Glu 415	Glu
Asn	Phe	Cys	Arg 420	Asn	Pro	Asp	Gly	Asp 425	Ser	His	Gly	Pro	Trp 430	Cys	Tyr
Thr	Met	Asp 435	Pro	Arg	Thr	Pro	Phe 440	Asp	Tyr	Cys	Ala	Leu 445	Arg	Arg	Cys
Ala	Asp 450	Asp	Gln	Pro	Pro	Ser 455	Ile	Leu	Asp	Pro	Pro 460	Asp	Gln	Val	Gln
Phe 465	Glu	Lys	Cys	Gly	Lys 470	Arg	Val	Asp	Arg	Leu 475	Asp	Gln	Arg	Arg	Ser 480
Lys	Leu	Arg	Val	Val 485	Gly	Gly	His	Pro	Gly 490	Asn	Ser	Pro	Trp	Thr 495	Val
Ser	Leu	Arg	Asn 500	Arg	Gln	Gly	Gln	His 505	Phe	Cys	Gly	Gly	Ser 510	Leu	Val
Lys	Glu	Gln 515	Trp	Ile	Leu	Thr	Ala 520	Arg	Gln	Cys	Phe	Ser 525	Ser	Cys	His
Met 530	Pro	Leu	Thr	Gly	Tyr	Glu 535	Val	Trp	Leu	Gly	Thr 540	Leu	Phe	Gln	Asn
Pro 545	Gln	His	Gly	Glu	Pro 550	Ser	Leu	Gln	Arg	Val 555	Pro	Val	Ala	Lys	Met 560
Val	Cys	Gly	Pro	Ser 565	Gly	Ser	Gln	Leu	Val 570	Leu	Leu	Lys	Leu	Glu 575	Arg
Ser	Val	Thr	Leu 580	Asn	Gln	Arg	Val	Ala 585	Leu	Ile	Cys	Leu	Pro 590	Pro	Glu
Trp	Tyr	Val 595	Val	Pro	Pro	Gly	Thr 600	Lys	Cys	Glu	Ile	Ala 605	Gly	Trp	Gly
Glu 610	Thr	Lys	Gly	Thr	Gly	Asn 615	Asp	Thr	Val	Leu	Asn 620	Val	Ala	Leu	Leu
Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Ile	Lys	His	Arg	Gly	Arg	Val



## Cura 468 SEQ list 0405.txt

625                      630                      635                      640

Arg Glu Ser Glu Met Cys Thr Glu Gly Leu Leu Ala Pro Val Gly Ala  
                                645                      650                      655

Cys Glu Gly Asp Tyr Gly Gly Pro Leu Ala Cys Phe Thr His Asn Cys  
                                660                      665                      670

Trp Val Leu Glu Gly Ile Ile Ile Pro Asn Arg Val Cys Ala Arg Ser  
                                675                      680                      685

Arg Trp Pro Ala Val Phe Thr Arg Val Ser Val Phe Val Asp Trp Ile  
                                690                      695                      700

His Lys Val Met Arg Leu Gly  
705                      710

<210> 54

<211> 529

<212> PRT

<213> Homo sapiens

<400> 54

Met Asp Cys Arg Ala Phe His Tyr Asn Val Ser Ser His Gly Cys Gln  
1                                  5                                  10                                  15

Leu Leu Pro Trp Thr Gln His Ser Pro His Thr Arg Leu Arg His Ser  
                                20                                  25                                  30

Gly Arg Cys Asp Leu Phe Gln Glu Lys Asp Tyr Ile Arg Thr Cys Ile  
                                35                                  40                                  45

Met Asn Asn Gly Val Gly Tyr Arg Gly Thr Met Ala Thr Thr Val Gly  
                                50                                  55                                  60

Gly Leu Ser Cys Gln Ala Trp Ser His Lys Phe Pro Asn Asp His Gln  
65                                  70                                  75                                  80

Tyr Met Pro Thr Leu Arg Asn Gly Leu Glu Glu Asn Phe Cys Arg Asn  
                                85                                  90                                  95

Pro Asp Gly Asp Pro Gly Gly Pro Trp Cys His Thr Thr Asp Pro Ala  
                                100                                  105                                  110

Val Arg Phe Gln Ser Cys Gly Ile Lys Ser Cys Arg Val Ala Ala Cys  
                                115                                  120                                  125

## Cura 468 SEQ list 0405.txt

Val	Trp	Cys	Asn	Gly	Glu	Glu	Tyr	Arg	Gly	Ala	Val	Asp	Arg	Thr	Glu
130						135					140				
Ser	Gly	Arg	Glu	Cys	Gln	Arg	Trp	Asp	Leu	Gln	His	Pro	His	Gln	His
145					150					155					160
Pro	Phe	Glu	Pro	Gly	Lys	Phe	Leu	Asp	Gln	Gly	Leu	Asp	Asp	Asn	Tyr
				165					170					175	
Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Arg	Pro	Trp	Cys	Tyr	Thr	Thr	Asp
			180					185					190		
Pro	Gln	Ile	Glu	Arg	Glu	Phe	Cys	Asp	Leu	Pro	Arg	Cys	Gly	Ser	Glu
		195					200					205			
Ala	Gln	Pro	Arg	Gln	Glu	Ala	Thr	Ser	Val	Ser	Cys	Phe	Arg	Gly	Lys
		210				215					220				
Gly	Glu	Gly	Tyr	Arg	Gly	Thr	Ala	Asn	Thr	Thr	Thr	Ala	Gly	Val	Pro
225					230					235					240
Cys	Gln	Arg	Trp	Asp	Ala	Gln	Ile	Pro	His	Gln	His	Arg	Phe	Thr	Pro
				245					250					255	
Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu	Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro
			260					265					270		
Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys	Phe	Thr	Leu	Arg	Pro	Gly	Met	Arg
		275					280					285			
Val	Gly	Phe	Cys	Tyr	Gln	Ile	Arg	Arg	Cys	Thr	Asp	Asp	Val	Arg	Pro
		290				295					300				
Gln	Asp	Cys	Tyr	His	Gly	Ala	Gly	Glu	Gln	Tyr	Arg	Gly	Thr	Val	Ser
305					310					315					320
Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys	Gln	Arg	Gly	Ser	Ala	Glu	Thr	Pro
				325					330					335	
His	Lys	Pro	Gln	Phe	Thr	Phe	Thr	Ser	Glu	Pro	His	Ala	Gln	Leu	Glu
			340					345					350		
Glu	Asn	Phe	Cys	Gln	Thr	Gln	Met	Gly	Ile	Ala	Met	Gly	Pro	Gly	Ala
		355					360					365			
Thr	Arg	Trp	Thr	Gln	Gly	Pro	His	Ser	Thr	Thr	Val	Pro	Cys	Asp	Ala
						375					380				

Cura 468 SEQ list 0405.txt

Ala	Leu	Met	Thr	Ser	Arg	His	Gln	Ser	Trp	Thr	Pro	Gln	Thr	Arg	Cys	
385					390					395					400	
Ser	Leu	Arg	Ser	Val	Ala	Arg	Gly	Trp	Ile	Gly	Trp	Ile	Ser	Val	Val	
				405					410					415		
Pro	Ser	Cys	Ala	Trp	Leu	Gly	Ala	Ile	Arg	Ala	Thr	His	Pro	Gly	Gln	
			420					425					430			
Ser	Ala	Cys	Gly	Ile	Gly	Gln	Gly	Gln	His	Phe	Cys	Gly	Gly	Ser	Leu	
		435					440					445				
Val	Lys	Glu	Gln	Trp	Ile	Leu	Thr	Ala	Arg	Gln	Cys	Phe	Ser	Ser	Cys	
	450					455					460					
His	Met	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	Thr	Leu	Phe	Gln	
465					470					475					480	
Asn	Pro	Gln	His	Gly	Glu	Pro	Gly	Leu	Gln	Arg	Val	Pro	Val	Ala	Lys	
				485					490					495		
Met	Leu	Cys	Gly	Pro	Ser	Gly	Ser	Gln	Leu	Val	Leu	Leu	Lys	Leu	Glu	
			500					505					510			
Arg	Ser	Val	Thr	Leu	Asn	Gln	Arg	Val	Ala	Leu	Ile	Cys	Leu	Pro	Pro	
		515					520					525				

Glu

<210> 55  
 <211> 716  
 <212> PRT  
 <213> Mus musculus

<400> 55																
Met	Gly	Trp	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Val	Gln	Cys	Ser	Arg	Ala	
1				5					10					15		
Leu	Gly	Gln	Arg	Ser	Pro	Leu	Asn	Asp	Phe	Gln	Leu	Phe	Arg	Gly	Thr	
			20					25					30			
Glu	Leu	Arg	Asn	Leu	Leu	His	Thr	Ala	Val	Pro	Gly	Pro	Trp	Gln	Glu	
		35					40					45				
Asp	Val	Ala	Asp	Ala	Glu	Glu	Cys	Ala	Arg	Arg	Cys	Gly	Pro	Leu	Leu	
	50					55					60					

## Cura 468 SEQ list 0405.txt

Asp 65	Cys	Arg	Ala	Phe	His 70	Tyr	Asn	Met	Ser	Ser 75	His	Gly	Cys	Gln	Leu 80
Leu	Pro	Trp	Thr	Gln 85	His	Ser	Leu	His	Thr 90	Gln	Leu	Tyr	His	Ser 95	Ser
Leu	Cys	His	Leu 100	Phe	Gln	Lys	Lys	Asp 105	Tyr	Val	Arg	Thr	Cys 110	Ile	Met
Asp	Asn	Gly 115	Val	Ser	Tyr	Arg	Gly 120	Thr	Val	Ala	Arg	Thr 125	Ala	Gly	Gly
Leu	Pro 130	Cys	Gln	Ala	Trp	Ser 135	Arg	Arg	Phe	Pro	Asn 140	Asp	His	Lys	Tyr
Thr 145	Pro	Thr	Pro	Lys	Asn 150	Gly	Leu	Glu	Glu	Asn 155	Phe	Cys	Arg	Asn	Pro 160
Asp	Gly	Asp	Pro	Arg 165	Gly	Pro	Trp	Cys	Tyr 170	Thr	Thr	Asn	Arg	Ser 175	Val
Arg	Phe	Gln	Ser 180	Cys	Gly	Ile	Lys	Thr 185	Cys	Arg	Glu	Ala	Val 190	Cys	Val
Leu	Cys	Asn 195	Gly	Glu	Asp	Tyr	Arg 200	Gly	Glu	Val	Asp 205	Val	Thr	Glu	Ser
Gly 210	Arg	Glu	Cys	Gln	Arg	Trp 215	Asp	Leu	Gln	His 220	Pro	His	Ser	His	Pro
Phe 225	Gln	Pro	Glu	Lys	Phe 230	Leu	Asp	Lys	Asp	Leu 235	Lys	Asp	Asn	Tyr	Cys 240
Arg	Asn	Pro	Asp	Gly 245	Ser	Glu	Arg	Pro	Trp 250	Cys	Tyr	Thr	Thr	Asp 255	Pro
Asn	Val	Glu	Arg 260	Glu	Phe	Cys	Asp	Leu 265	Pro	Ser	Cys	Gly	Pro 270	Asn	Leu
Pro	Pro	Thr 275	Val	Lys	Gly	Ser	Lys 280	Ser	Gln	Arg	Arg	Asn 285	Lys	Gly	Lys
Ala 290	Leu	Asn	Cys	Phe	Arg	Gly 295	Lys	Gly	Glu	Asp	Tyr 300	Arg	Gly	Thr	Thr
Asn 305	Thr	Thr	Ser	Ala	Gly 310	Val	Pro	Cys	Gln	Arg 315	Trp	Asp	Ala	Gln	Ser 320

Cura 468 SEQ list 0405.txt

Pro	His	Gln	His	Arg	Phe	Val	Pro	Glu	Lys	Tyr	Ala	Cys	Lys	Asp	Leu	325	330	335
Arg	Glu	Asn	Phe	Cys	Arg	Asn	Pro	Asp	Gly	Ser	Glu	Ala	Pro	Trp	Cys	340	345	350
Phe	Thr	Ser	Arg	Pro	Gly	Leu	Arg	Met	Ala	Phe	Cys	His	Gln	Ile	Pro	355	360	365
Arg	Cys	Thr	Glu	Glu	Leu	Val	Pro	Glu	Gly	Cys	Tyr	His	Gly	Ser	Gly	370	375	380
Glu	Gln	Tyr	Arg	Gly	Ser	Val	Ser	Lys	Thr	Arg	Lys	Gly	Val	Gln	Cys	385	390	395
Gln	His	Trp	Ser	Ser	Glu	Thr	Pro	His	Lys	Pro	Gln	Phe	Thr	Pro	Thr	405	410	415
Ser	Ala	Pro	Gln	Ala	Gly	Leu	Glu	Ala	Asn	Phe	Cys	Arg	Asn	Pro	Asp	420	425	430
Gly	Asp	Ser	His	Gly	Pro	Trp	Cys	Tyr	Thr	Leu	Asp	Pro	Asp	Ile	Leu	435	440	445
Phe	Asp	Tyr	Cys	Ala	Leu	Gln	Arg	Cys	Asp	Asp	Asp	Gln	Pro	Pro	Ser	450	455	460
Ile	Leu	Asp	Pro	Pro	Asp	Gln	Val	Val	Phe	Glu	Lys	Cys	Gly	Lys	Arg	465	470	475
Val	Asp	Lys	Ser	Asn	Lys	Leu	Arg	Val	Val	Gly	Gly	His	Pro	Gly	Asn	485	490	495
Ser	Pro	Trp	Thr	Val	Ser	Leu	Arg	Asn	Arg	Gln	Gly	Gln	His	Phe	Cys	500	505	510
Gly	Gly	Ser	Leu	Val	Lys	Glu	Gln	Trp	Val	Leu	Thr	Ala	Arg	Gln	Cys	515	520	525
Ile	Trp	Ser	Cys	His	Glu	Pro	Leu	Thr	Gly	Tyr	Glu	Val	Trp	Leu	Gly	530	535	540
Thr	Ile	Asn	Gln	Asn	Pro	Gln	Pro	Gly	Glu	Ala	Asn	Leu	Gln	Arg	Val	545	550	555
Pro	Val	Ala	Lys	Ala	Val	Cys	Gly	Pro	Ala	Gly	Ser	Gln	Leu	Val	Leu	565	570	575

Cura 468 SEQ list 0405.txt

Leu	Lys	Leu	Glu	Arg	Pro	Val	Ile	Leu	Asn	His	His	Val	Ala	Leu	Ile	
			580					585					590			
Cys	Leu	Pro	Pro	Glu	Gln	Tyr	Val	Val	Pro	Pro	Gly	Thr	Lys	Cys	Glu	
		595					600					605				
Ile	Ala	Gly	Trp	Gly	Glu	Ser	Ile	Gly	Thr	Ser	Asn	Asn	Thr	Val	Leu	
	610					615					620					
His	Val	Ala	Ser	Met	Asn	Val	Ile	Ser	Asn	Gln	Glu	Cys	Asn	Thr	Lys	
625					630					635					640	
Tyr	Arg	Gly	His	Ile	Gln	Glu	Ser	Glu	Ile	Cys	Thr	Gln	Gly	Leu	Val	
				645					650					655		
Val	Pro	Val	Gly	Ala	Cys	Glu	Gly	Asp	Tyr	Gly	Gly	Pro	Leu	Ala	Cys	
			660					665					670			
Tyr	Thr	His	Asp	Cys	Trp	Val	Leu	Gln	Gly	Leu	Ile	Ile	Pro	Asn	Arg	
		675					680					685				
Val	Cys	Ala	Arg	Pro	Arg	Trp	Pro	Ala	Ile	Phe	Thr	Arg	Val	Ser	Val	
	690					695					700					
Phe	Val	Asp	Trp	Ile	Asn	Lys	Val	Met	Gln	Leu	Glu					
705					710					715						

<210> 56  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 56

Met	Ala	Thr	Val	Gln	Gln	Leu	Glu	Gly	Arg	Trp	Arg	Leu	Val	Asp	Ser	
1				5					10					15		
Lys	Gly	Phe	Asp	Glu	Tyr	Met	Lys	Glu	Leu	Gly	Val	Gly	Ile	Ala	Leu	
			20					25					30			
Arg	Lys	Met	Gly	Ala	Met	Ala	Lys	Pro	Asp	Cys	Ile	Val	Thr	Cys	Asp	
		35					40					45				
Gly	Lys	Asn	Leu	Thr	Ile	Lys	Thr	Glu	Ser	Thr	Leu	Lys	Thr	Thr	Gln	
	50					55					60					
Phe	Ser	Cys	Pro	Leu	Gly	Glu	Lys	Phe	Glu	Glu	Thr	Thr	Ala	Asp	Gly	

65		70		75		80									
Arg	Lys	Thr	Gln	Thr	Val	Cys	Asn	Phe	Thr	Asp	Gly	Ala	Leu	Val	Gln
				85					90					95	
His	Gln	Glu	Trp	Asp	Gly	Lys	Glu	Ser	Thr	Ile	Thr	Arg	Lys	Leu	Lys
			100					105					110		
Asp	Gly	Lys	Leu	Val	Val	Glu	Cys	Val	Met	Asn	His	Val	Ala	Cys	Thr
		115					120					125			
Arg	Ile	Tyr	Glu	Lys	Val	Glu									
	130					135									
<210>	57														
<211>	135														
<212>	PRT														
<213>	Homo sapiens														
<400>	57														
Met	Ala	Thr	Val	Gln	Gln	Leu	Glu	Gly	Arg	Trp	Arg	Leu	Val	Asp	Ser
1				5					10					15	
Lys	Gly	Phe	Asp	Glu	Tyr	Met	Lys	Glu	Leu	Gly	Val	Gly	Ile	Ala	Leu
			20					25					30		
Arg	Lys	Met	Gly	Ala	Met	Ala	Lys	Pro	Asp	Cys	Ile	Ile	Thr	Cys	Asp
		35					40					45			
Gly	Lys	Asn	Leu	Thr	Ile	Lys	Thr	Glu	Ser	Thr	Leu	Lys	Thr	Thr	Gln
	50					55					60				
Phe	Ser	Cys	Thr	Leu	Gly	Glu	Lys	Phe	Glu	Glu	Thr	Thr	Ala	Asp	Gly
65					70					75					80
Arg	Lys	Thr	Gln	Thr	Val	Cys	Asn	Phe	Thr	Asp	Gly	Ala	Leu	Val	Gln
				85					90					95	
His	Gln	Glu	Trp	Asp	Gly	Lys	Glu	Ser	Thr	Ile	Thr	Arg	Lys	Leu	Lys
			100					105					110		
Asp	Gly	Lys	Leu	Val	Val	Glu	Cys	Val	Met	Asn	Asn	Val	Thr	Cys	Thr
		115					120					125			
Arg	Ile	Tyr	Glu	Lys	Val	Glu									
	130					135									

Cura 468 SEQ list 0405.txt

<210> 58  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 58  
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Val Asp Ser  
 1 5 10 15  
 Arg Gly Phe Asp Glu Tyr Val Lys Glu Leu Gly Val Gly Ile Ala Leu  
 20 25 30  
 Arg Lys Met Asp Thr Ile Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp  
 35 40 45  
 Gly Lys Asn Leu Thr Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln  
 50 55 60  
 Phe Ser Cys Thr Leu Gly Glu Asn Phe Glu Glu Thr Thr Ala Asp Gly  
 65 70 75 80  
 Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln  
 85 90 95  
 His Gln Glu Trp Asp Gly Lys Glu Asn Thr Ile Arg Arg Lys Leu Lys  
 100 105 110  
 Asp Gly Lys Leu Val Val Asp Cys Val Met Asn Ser Val Thr Cys Thr  
 115 120 125  
 Arg Ile Tyr Glu Lys Val Glu  
 130 135

<210> 59  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

<400> 59  
 Met Ala Thr Val Gln Gln Leu Glu Gly Arg Trp Arg Leu Leu Asp Ser  
 1 5 10 15  
 Lys Gly Phe Asp Glu Tyr Met Lys Glu Leu Gly Val Gly Ile Ala Leu  
 20 25 30  
 Gln Lys Met Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Cys Asp



## Cura 468 SEQ list 0405.txt

35

40

45

Gly Arg Asn Leu Thr Thr Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln  
           50                          55                          60

Phe Ser Cys Thr Leu Gly Asp Glu Phe Glu Glu Thr Thr Ala Asp Gly  
       65                          70                          75                          80

Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln  
                           85                          90                          95

His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Lys  
                           100                          105                          110

Asp Gly Lys Leu Val Val Glu Cys Val Met Asn Asn Val Thr Cys Thr  
           115                          120                          125

Arg Ile Tyr Glu Lys Val Glu  
       130                          135

&lt;210&gt; 60

&lt;211&gt; 135

&lt;212&gt; PRT

&lt;213&gt; Bos taurus

&lt;400&gt; 60

Met Ala Thr Val Gln Gln Leu Val Gly Arg Trp Arg Leu Val Glu Ser  
       1                          5                          10                          15

Lys Gly Phe Asp Glu Tyr Met Lys Glu Val Gly Val Gly Met Ala Leu  
                           20                          25                          30

Arg Lys Val Gly Ala Met Ala Lys Pro Asp Cys Ile Ile Thr Ser Asp  
           35                          40                          45

Gly Lys Asn Leu Ser Ile Lys Thr Glu Ser Thr Leu Lys Thr Thr Gln  
       50                          55                          60

Phe Ser Cys Lys Leu Gly Glu Lys Phe Glu Glu Thr Thr Ala Asp Gly  
       65                          70                          75                          80

Arg Lys Thr Gln Thr Val Cys Asn Phe Thr Asp Gly Ala Leu Val Gln  
                           85                          90                          95

His Gln Glu Trp Asp Gly Lys Glu Ser Thr Ile Thr Arg Lys Leu Glu  
                           100                          105                          110

Cura 468 SEQ list 0405.txt

Asp Gly Lys Leu Val Val Val Cys Val Met Asn Asn Val Thr Cys Thr  
115 120 125

Arg Val Tyr Glu Lys Val Glu  
130 135

<210> 61

<211> 266

<212> PRT

<213> Homo sapiens

<400> 61

Met Asn Trp Ala Phe Leu Gln Gly Leu Leu Ser Gly Val Asn Lys Tyr  
1 5 10 15

Ser Thr Val Leu Ser Arg Ile Trp Leu Ser Val Val Phe Ile Phe Arg  
20 25 30

Val Leu Val Tyr Val Val Ala Ala Glu Glu Val Trp Asp Asp Glu Gln  
35 40 45

Lys Asp Phe Val Cys Asn Thr Lys Gln Pro Gly Cys Pro Asn Val Cys  
50 55 60

Tyr Asp Glu Phe Phe Pro Val Ser His Val Arg Leu Trp Ala Leu Gln  
65 70 75 80

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
85 90 95

Tyr Arg Glu Glu Arg Glu Arg Lys His His Leu Lys His Gly Pro Asn  
100 105 110

Ala Pro Ser Leu Tyr Asp Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp  
115 120 125

Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ala Gly  
130 135 140

Phe Leu Tyr Ile Phe His Arg Leu Tyr Lys Asp Tyr Asp Met Pro Arg  
145 150 155 160

Val Val Ala Cys Ser Val Glu Pro Cys Pro His Thr Val Asp Cys Tyr  
165 170 175

Ile Ser Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Thr  
180 185 190

Cura 468 SEQ list 0405.txt

Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Ser	Glu	Val	Phe	Tyr	Leu
		195					200					205			
Val	Gly	Lys	Arg	Cys	Met	Glu	Ile	Phe	Gly	Pro	Arg	His	Arg	Arg	Pro
	210					215					220				
Arg	Cys	Arg	Glu	Cys	Leu	Pro	Asp	Thr	Cys	Pro	Pro	Tyr	Val	Leu	Ser
225					230					235					240
Gln	Gly	Gly	His	Pro	Glu	Asp	Gly	Asn	Ser	Val	Leu	Met	Lys	Ala	Gly
				245					250					255	
Ser	Ala	Pro	Val	Asp	Ala	Gly	Gly	Tyr	Pro						
			260					265							

<210> 62  
 <211> 265  
 <212> PRT  
 <213> Rattus norvegicus

<400> 62

Met	Asn	Trp	Gly	Phe	Leu	Gln	Gly	Ile	Leu	Ser	Gly	Val	Asn	Lys	Tyr
1				5					10					15	
Ser	Thr	Ala	Leu	Gly	Arg	Ile	Trp	Leu	Ser	Val	Val	Phe	Ile	Phe	Arg
			20					25					30		
Val	Leu	Val	Tyr	Val	Val	Ala	Ala	Glu	Glu	Val	Trp	Asp	Asp	Glu	Gln
		35					40					45			
Lys	Asp	Phe	Ile	Cys	Asn	Thr	Lys	Gln	Pro	Gly	Cys	Pro	Asn	Val	Cys
	50					55					60				
Tyr	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln
65					70					75					80
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala
				85					90					95	
Tyr	Arg	Glu	Glu	Arg	Glu	Arg	Lys	His	Arg	Leu	Lys	His	Gly	Pro	Asp
			100					105					110		
Ala	Pro	Ala	Leu	Tyr	Ser	Asn	Leu	Ser	Lys	Lys	Arg	Gly	Gly	Leu	Trp
		115					120					125			
Trp	Thr	Tyr	Leu	Leu	Ser	Leu	Ile	Phe	Lys	Ala	Ala	Val	Asp	Ser	Gly

## Cura 468 SEQ list 0405.txt

130

135

140

Phe 145	Leu	Tyr	Ile	Phe 150	His	Cys	Ile	Tyr	Lys	Asp 155	Tyr	Asp	Met	Pro	Arg 160
Val	Val	Ala	Cys	Ser 165	Val	Gln	Pro	Cys	Pro 170	His	Thr	Val	Asp	Cys 175	Tyr
Ile	Ser	Arg	Pro 180	Thr	Glu	Lys	Lys	Val 185	Phe	Thr	Tyr	Phe	Met 190	Val	Val
Thr	Ala	Ala 195	Ile	Cys	Ile	Leu	Leu 200	Asn	Leu	Ser	Glu	Val 205	Ala	Tyr	Leu
Val	Gly 210	Lys	Arg	Cys	Met	Glu 215	Val	Phe	Arg	Pro	Arg 220	Arg	Gln	Lys	Thr
Ser 225	Arg	Arg	His	Gln	Leu 230	Pro	Asp	Thr	Cys	Pro 235	Pro	Tyr	Val	Ile	Ser 240
Lys	Gly	His	Pro	Gln 245	Asp	Glu	Ser	Thr	Val 250	Leu	Thr	Lys	Ala	Gly 255	Met
Ala	Thr	Val	Asp 260	Ala	Gly	Val	Tyr	Pro 265							

&lt;210&gt; 63

&lt;211&gt; 266

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 63

Met 1	Asn	Trp	Gly	Phe 5	Leu	Gln	Gly	Ile	Leu 10	Ser	Gly	Val	Asn	Lys 15	Tyr
Ser	Thr	Ala	Leu 20	Gly	Arg	Ile	Trp	Leu 25	Ser	Val	Val	Phe	Ile 30	Phe	Arg
Val	Leu	Val 35	Tyr	Val	Val	Ala	Ala 40	Glu	Glu	Val	Trp	Asp 45	Asp	Asp	Gln
Lys	Asp 50	Phe	Ile	Cys	Asn	Thr 55	Lys	Gln	Pro	Gly	Cys 60	Pro	Asn	Val	Cys
Tyr 65	Asp	Glu	Phe	Phe	Pro 70	Val	Ser	His	Val	Arg 75	Leu	Trp	Ala	Leu	Gln 80

Cura 468 SEQ list 0405.txt

Leu Ile Leu Val Thr Cys Pro Ser Leu Leu Val Val Met His Val Ala  
85 90 95

Tyr Arg Glu Glu Arg Glu Arg Lys His Arg Leu Lys His Gly Pro Asn  
100 105 110

Ala Pro Ala Leu Tyr Ser Asn Leu Ser Lys Lys Arg Gly Gly Leu Trp  
115 120 125

Trp Thr Tyr Leu Leu Ser Leu Ile Phe Lys Ala Ala Val Asp Ser Gly  
130 135 140

Phe Leu Tyr Ile Phe His Cys Ile Tyr Lys Asp Tyr Asp Met Pro Arg  
145 150 155 160

Val Val Ala Cys Ser Val Thr Pro Cys Pro His Thr Val Asp Cys Tyr  
165 170 175

Ile Ala Arg Pro Thr Glu Lys Lys Val Phe Thr Tyr Phe Met Val Val  
180 185 190

Thr Ala Ala Ile Cys Ile Leu Leu Asn Leu Ser Glu Val Val Tyr Leu  
195 200 205

Val Gly Lys Arg Cys Met Glu Val Phe Arg Pro Arg Arg Arg Lys Ala  
210 215 220

Ser Arg Arg His Gln Leu Pro Asp Thr Cys Pro Pro Tyr Val Ile Ser  
225 230 235 240

Lys Gly Gly His Pro Gln Asp Glu Ser Val Ile Leu Thr Lys Ala Gly  
245 250 255

Met Ala Thr Val Asp Ala Gly Val Tyr Pro  
260 265

<210> 64

<211> 273

<212> PRT

<213> Homo sapiens

<400> 64

Met Asn Trp Ser Ile Phe Glu Gly Leu Leu Ser Gly Val Asn Lys Tyr  
1 5 10 15

Ser Thr Ala Phe Gly Arg Ile Trp Leu Ser Leu Val Phe Ile Phe Arg  
20 25 30

Cura 468 SEQ list 0405.txt

Val	Leu	Val	Tyr	Leu	Val	Thr	Ala	Glu	Arg	Val	Trp	Ser	Asp	Asp	His
		35					40					45			
Lys	Asp	Phe	Asp	Cys	Asn	Thr	Arg	Gln	Pro	Gly	Cys	Ser	Asn	Val	Cys
	50					55					60				
Phe	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln
65					70					75					80
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala
				85					90					95	
Tyr	Arg	Glu	Val	Gln	Glu	Lys	Arg	His	Arg	Glu	Ala	His	Gly	Glu	Asn
			100					105					110		
Ser	Gly	Arg	Leu	Tyr	Leu	Asn	Pro	Gly	Lys	Lys	Arg	Gly	Gly	Leu	Trp
		115					120					125			
Trp	Thr	Tyr	Val	Cys	Ser	Leu	Val	Phe	Lys	Ala	Ser	Val	Asp	Ile	Ala
	130					135					140				
Phe	Leu	Tyr	Val	Phe	His	Ser	Phe	Tyr	Pro	Lys	Tyr	Ile	Leu	Pro	Pro
145					150					155					160
Val	Val	Lys	Cys	His	Ala	Asp	Pro	Cys	Pro	Asn	Ile	Val	Asp	Cys	Phe
				165					170					175	
Ile	Ser	Lys	Pro	Ser	Glu	Lys	Asn	Ile	Phe	Thr	Leu	Phe	Met	Val	Ala
			180					185					190		
Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	Ile	Tyr	Leu
		195					200					205			
Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	Ala	Gln	Ala
	210					215					220				
Met	Cys	Thr	Gly	His	His	Pro	His	Gly	Thr	Thr	Ser	Ser	Cys	Lys	Gln
225					230					235					240
Asp	Asp	Leu	Leu	Ser	Gly	Asp	Leu	Ile	Phe	Leu	Gly	Ser	Asp	Ser	His
				245					250					255	
Pro	Pro	Leu	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	Lys	Thr	Ile
			260					265					270		
Leu															

<210> 65  
 <211> 273  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> VARIANT  
 <222> (41)  
 <223> Wherein Xaa is any amino acid.

<400> 65

Met	Asn	Trp	Ser	Ile	Phe	Glu	Gly	Leu	Leu	Ser	Gly	Val	Asn	Lys	Tyr	1	5	10	15
Ser	Thr	Ala	Phe	Gly	Arg	Ile	Trp	Leu	Ser	Leu	Val	Phe	Ile	Phe	Arg	20	25	30	
Val	Leu	Val	Tyr	Leu	Val	Thr	Ala	Xaa	Arg	Val	Trp	Ser	Asp	Asp	His	35	40	45	
Lys	Asp	Phe	Asp	Cys	Asn	Thr	Arg	Gln	Pro	Gly	Cys	Ser	Asn	Val	Cys	50	55	60	
Phe	Asp	Glu	Phe	Phe	Pro	Val	Ser	His	Val	Arg	Leu	Trp	Ala	Leu	Gln	65	70	75	80
Leu	Ile	Leu	Val	Thr	Cys	Pro	Ser	Leu	Leu	Val	Val	Met	His	Val	Ala	85	90	95	
Tyr	Arg	Glu	Val	Gln	Glu	Lys	Arg	His	Arg	Glu	Ala	His	Gly	Glu	Asn	100	105	110	
Ser	Gly	Arg	Leu	Tyr	Leu	Asn	Pro	Gly	Lys	Lys	Arg	Gly	Gly	Leu	Trp	115	120	125	
Trp	Thr	Tyr	Val	Cys	Ser	Leu	Val	Phe	Lys	Ala	Ser	Val	Asp	Ile	Ala	130	135	140	
Phe	Leu	Tyr	Val	Phe	His	Ser	Phe	Tyr	Pro	Lys	Tyr	Ile	Leu	Pro	Pro	145	150	155	160
Val	Val	Lys	Cys	His	Ala	Asp	Pro	Cys	Pro	Asn	Ile	Val	Asp	Cys	Phe	165	170	175	
Ile	Ser	Lys	Pro	Ser	Glu	Lys	Asn	Ile	Phe	Thr	Leu	Phe	Met	Val	Ala	180	185	190	

Cura 468 SEQ list 0405.txt

Thr	Ala	Ala	Ile	Cys	Ile	Leu	Leu	Asn	Leu	Val	Glu	Leu	Ile	Tyr	Leu
		195					200					205			
Val	Ser	Lys	Arg	Cys	His	Glu	Cys	Leu	Ala	Ala	Arg	Lys	Ala	Gln	Ala
	210					215					220				
Met	Cys	Thr	Gly	His	His	Pro	His	Gly	Thr	Thr	Ser	Ser	Cys	Lys	Gln
225					230					235					240
Asp	Asp	Leu	Leu	Ser	Gly	Asp	Leu	Ile	Phe	Leu	Gly	Ser	Asp	Ser	His
				245					250					255	
Pro	Pro	Leu	Leu	Pro	Asp	Arg	Pro	Arg	Asp	His	Val	Lys	Lys	Thr	Ile
			260					265					270		

Leu

<210> 66  
 <211> 434  
 <212> PRT  
 <213> Homo sapiens

<400> 66

Ala	Lys	Gln	Gln	Leu	Asn	Leu	Arg	Thr	His	Met	Ala	Asp	Glu	Asn	Lys
1				5					10					15	
Asn	Glu	Tyr	Ala	Ala	Gln	Leu	Gln	Asn	Phe	Asn	Gly	Glu	Gln	His	Lys
			20					25					30		
His	Phe	Tyr	Val	Val	Ile	Pro	Gln	Ile	Tyr	Lys	Gln	Leu	Gln	Glu	Met
		35					40					45			
Asp	Glu	Arg	Arg	Thr	Ile	Lys	Leu	Ser	Glu	Cys	Tyr	Arg	Gly	Phe	Ala
	50					55					60				
Asp	Ser	Glu	Arg	Lys	Val	Ile	Pro	Ile	Ile	Ser	Lys	Cys	Leu	Glu	Gly
65					70					75					80
Met	Ile	Leu	Ala	Ala	Lys	Ser	Val	Asp	Glu	Arg	Arg	Asp	Ser	Gln	Met
				85					90					95	
Val	Val	Asp	Ser	Phe	Lys	Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Phe	Pro
			100					105					110		
Phe	Glu	Asp	Tyr	Ser	Gln	His	Ile	Tyr	Arg	Thr	Ile	Ser	Asp	Gly	Thr



## Cura 468 SEQ list 0405.txt

115					120					125					
Ile	Ser	Ala	Ser	Lys	Gln	Glu	Ser	Gly	Lys	Met	Asp	Ala	Lys	Thr	Thr
	130					135					140				
Val	Gly	Lys	Ala	Lys	Gly	Lys	Leu	Trp	Leu	Phe	Gly	Lys	Lys	Pro	Lys
145					150					155					160
Pro	Gln	Ser	Pro	Pro	Leu	Thr	Pro	Thr	Ser	Leu	Phe	Thr	Ser	Ser	Thr
				165					170					175	
Pro	Asn	Gly	Ser	Gln	Phe	Leu	Thr	Phe	Ser	Ile	Glu	Pro	Val	His	Tyr
			180					185					190		
Cys	Met	Asn	Glu	Ile	Lys	Thr	Gly	Lys	Pro	Arg	Ile	Pro	Ser	Phe	Arg
		195					200					205			
Ser	Leu	Lys	Arg	Gly	Gly	Pro	Ala	Leu	Glu	Asp	Phe	Ser	His	Leu	Pro
	210					215					220				
Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Arg	Ile	Asp	Glu	Leu	Asn
225					230					235					240
Arg	Glu	Leu	Gln	Lys	Glu	Ser	Asp	Gln	Lys	Asp	Ala	Leu	Asn	Lys	Met
				245					250					255	
Lys	Asp	Val	Tyr	Glu	Lys	Asn	Pro	Gln	Met	Gly	Asp	Pro	Gly	Ser	Leu
			260					265					270		
Gln	Pro	Lys	Leu	Ala	Glu	Thr	Met	Asn	Asn	Ile	Asp	Arg	Leu	Arg	Met
		275					280					285			
Glu	Ile	His	Lys	Asn	Glu	Ala	Trp	Leu	Ser	Glu	Val	Glu	Gly	Lys	Thr
	290					295					300				
Gly	Gly	Arg	Gly	Asp	Arg	Arg	His	Ser	Ser	Asp	Ile	Asn	His	Leu	Val
305					310					315					320
Thr	Gln	Gly	Arg	Glu	Ser	Pro	Glu	Gly	Ser	Tyr	Thr	Asp	Asp	Ala	Asn
				325					330					335	
Gln	Glu	Val	Arg	Gly	Pro	Pro	Gln	Gln	His	Gly	His	His	Asn	Glu	Phe
			340					345					350		
Asp	Asp	Glu	Phe	Glu	Asp	Asp	Asp	Pro	Leu	Pro	Ala	Ile	Gly	His	Cys
		355					360					365			
Lys	Ala	Ile	Tyr	Pro	Phe	Asp	Gly	His	Asn	Glu	Gly	Thr	Leu	Ala	Met

Cura 468 SEQ list 0405.txt

370

375

380

Lys Glu Gly Glu Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly  
385 390 395 400

Trp Thr Arg Ala Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr  
405 410 415

Ser Tyr Ile Asp Val Thr Leu Glu Lys Asn Ser Lys Gly Ala Val Thr  
420 425 430

Tyr Ile

<210> 67

<211> 330

<212> PRT

<213> Homo sapiens

<400> 67

Met Asp Glu Arg Arg Thr Ile Lys Leu Ser Glu Cys Tyr Arg Gly Phe  
1 5 10 15

Ala Asp Ser Glu Arg Lys Val Ile Pro Ile Ile Ser Lys Cys Leu Glu  
20 25 30

Gly Met Ile Leu Ala Ala Lys Ser Val Asp Glu Arg Arg Asp Ser Gln  
35 40 45

Met Val Val Asp Ser Phe Lys Ser Gly Phe Glu Pro Pro Gly Asp Phe  
50 55 60

Pro Phe Glu Asp Tyr Ser Gln His Ile Tyr Arg Thr Ile Ser Asp Gly  
65 70 75 80

Thr Ile Ser Ala Ser Lys Gln Glu Ser Gly Lys Met Asp Ala Lys Thr  
85 90 95

Thr Val Gly Lys Ala Lys Gly Lys Leu Trp Leu Phe Gly Lys Lys Pro  
100 105 110

Lys Gly Pro Ala Leu Glu Asp Phe Ser His Leu Pro Pro Glu Gln Arg  
115 120 125

Arg Lys Lys Leu Gln Gln Arg Ile Asp Glu Leu Asn Arg Glu Leu Gln  
130 135 140

Cura 468 SEQ list 0405.txt

Lys Glu Ser Asp Gln Lys Asp Ala Leu Asn Lys Met Lys Asp Val Tyr  
145 150 155 160

Glu Lys Asn Pro Gln Met Gly Asp Pro Gly Ser Leu Gln Pro Lys Leu  
165 170 175

Ala Glu Thr Met Asn Asn Ile Asp Arg Leu Arg Met Glu Ile His Lys  
180 185 190

Asn Glu Ala Trp Leu Ser Glu Val Glu Gly Lys Thr Gly Gly Arg Gly  
195 200 205

Asp Arg Arg His Ser Ser Asp Ile Asn His Leu Val Thr Gln Gly Arg  
210 215 220

Glu Ser Pro Glu Gly Ser Tyr Thr Asp Asp Ala Asn Gln Glu Val Arg  
225 230 235 240

Gly Pro Pro Gln Gln His Gly His His Asn Glu Phe Asp Asp Glu Phe  
245 250 255

Glu Asp Asp Asp Pro Leu Pro Ala Ile Gly His Cys Lys Ala Ile Tyr  
260 265 270

Pro Phe Asp Gly His Asn Glu Gly Thr Leu Ala Met Lys Glu Gly Glu  
275 280 285

Val Leu Tyr Ile Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ala  
290 295 300

Arg Arg Gln Asn Gly Glu Glu Gly Tyr Val Pro Thr Ser Tyr Ile Asp  
305 310 315 320

Val Thr Leu Glu Lys Asn Ser Lys Gly Ser  
325 330

<210> 68

<211> 592

<212> PRT

<213> Homo sapiens

<400> 68

Met Ser Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys  
1 5 10 15

His Thr Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val  
20 25 30

Cura 468 SEQ list 0405.txt

Lys	Glu	Arg	Thr	Glu	Ile	Glu	Leu	Ser	Tyr	Ala	Lys	Gln	Leu	Arg	Asn
		35					40					45			
Leu	Ser	Lys	Lys	Tyr	Gln	Pro	Lys	Lys	Asn	Ser	Lys	Glu	Glu	Glu	Glu
	50					55					60				
Tyr	Lys	Tyr	Thr	Ser	Cys	Lys	Ala	Phe	Ile	Ser	Asn	Leu	Asn	Glu	Met
65					70					75					80
Asn	Asp	Tyr	Ala	Gly	Gln	His	Glu	Val	Ile	Ser	Glu	Asn	Met	Ala	Ser
				85					90					95	
Gln	Ile	Ile	Val	Asp	Leu	Ala	Arg	Tyr	Val	Gln	Glu	Leu	Lys	Gln	Glu
			100					105					110		
Arg	Lys	Ser	Asn	Phe	His	Asp	Gly	Arg	Lys	Ala	Gln	Gln	His	Ile	Glu
		115					120					125			
Thr	Cys	Trp	Lys	Gln	Leu	Glu	Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp
	130					135					140				
Cys	Lys	Glu	Ala	Asp	Arg	Ala	Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala
145					150					155					160
Asp	Ile	Asn	Val	Thr	Lys	Ala	Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala
				165					170					175	
Gln	Ile	Arg	His	Gln	Met	Ala	Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser
			180					185					190		
Ile	Leu	Gln	Lys	Phe	Asn	His	Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His
		195					200					205			
Ile	Pro	Asn	Ile	Phe	Gln	Lys	Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile
	210					215					220				
Val	Arg	Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln
225					230					235					240
Val	Ile	Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala
				245					250					255	
Glu	Ser	Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr
			260					265					270		
Lys	Ser	Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr
		275					280					285			

## Cura 468 SEQ list 0405.txt

Gln	Pro	Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	290	295	300
Gly	Glu	Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	305	310	315
Leu	Trp	Pro	Phe	Ile	Lys	Lys	Asn	Lys	Ser	Pro	Lys	Gln	Gln	Lys	Glu	325	330	335
Pro	Leu	Ser	His	Arg	Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile	340	345	350
His	Cys	Phe	Arg	Ser	Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala	355	360	365
Thr	Pro	Glu	Asp	Phe	Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	370	375	380
Leu	Gln	Gln	Lys	Val	Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met	385	390	395
Asp	Gln	Arg	Asp	Ala	Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn	405	410	415
Pro	Gln	Met	Gly	Asp	Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val	420	425	430
Ser	Gln	Asn	Ile	Glu	Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala	435	440	445
Trp	Leu	Ala	Glu	Val	Glu	Gly	Arg	Leu	Pro	Ala	Arg	Asn	Glu	Gln	Ala	450	455	460
Arg	Arg	Gln	Ser	Gly	Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn	465	470	475
Asn	Cys	Ala	Gln	Asp	Arg	Glu	Ser	Pro	Asp	Gly	Ser	Tyr	Thr	Glu	Glu	485	490	495
Gln	Ser	Gln	Glu	Ser	Glu	Met	Lys	Val	Leu	Ala	Thr	Asp	Phe	Asp	Asp	500	505	510
Glu	Phe	Asp	Asp	Glu	Glu	Pro	Leu	Pro	Ala	Ile	Gly	Thr	Cys	Lys	Ala	515	520	525
Leu	Tyr	Thr	Phe	Glu	Gly	Gln	Asn	Glu	Gly	Thr	Ile	Ser	Val	Val	Glu	530	535	540

Cura 468 SEQ list 0405.txt

Gly Glu Thr Leu Tyr Val Ile Glu Glu Asp Lys Gly Asp Gly Trp Thr  
545 550 555 560

Arg Ile Arg Arg Asn Glu Asp Glu Glu Gly Tyr Val Pro Thr Ser Tyr  
565 570 575

Val Glu Val Cys Leu Asp Lys Asn Ala Lys Gly Ala Lys Thr Tyr Ile  
580 585 590

<210> 69

<211> 679

<212> PRT

<213> Homo sapiens

<400> 69

Leu Trp Asn Gly Gly Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg  
1 5 10 15

Ser Cys Glu Pro Glu Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser  
20 25 30

Arg Gly Ser Arg Gly Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu  
35 40 45

Pro Arg Pro Pro Arg Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser  
50 55 60

Trp Gly Thr Glu Leu Trp Asp Gln Phe Asp Asn Leu Glu Lys His Thr  
65 70 75 80

Gln Trp Gly Ile Asp Ile Leu Glu Lys Tyr Ile Lys Phe Val Lys Glu  
85 90 95

Arg Thr Glu Ile Glu Leu Ser Tyr Ala Lys Gln Leu Arg Asn Leu Ser  
100 105 110

Lys Lys Tyr Gln Pro Lys Lys Asn Ser Lys Glu Glu Glu Glu Tyr Lys  
115 120 125

Tyr Thr Ser Cys Lys Ala Phe Ile Ser Asn Leu Asn Glu Met Asn Asp  
130 135 140

Tyr Ala Gly Gln His Glu Val Ile Ser Glu Asn Met Ala Ser Gln Ile

## Cura 468 SEQ list 0405.txt

145					150					155						160
Ile	Val	Asp	Leu	Ala	Arg	Tyr	Val	Gln	Glu	Leu	Lys	Gln	Glu	Arg	Lys	
				165					170					175		
Ser	Asn	Phe	His	Asp	Gly	Arg	Lys	Ala	Gln	Gln	His	Ile	Glu	Thr	Cys	
			180					185					190			
Trp	Lys	Gln	Leu	Glu	Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	Cys	Lys	
		195					200					205				
Glu	Ala	Asp	Arg	Ala	Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	Asp	Ile	
	210					215					220					
Asn	Val	Thr	Lys	Ala	Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	Gln	Ile	
225					230					235					240	
Arg	His	Gln	Met	Ala	Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	Ile	Leu	
				245					250					255		
Gln	Lys	Phe	Asn	His	Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	Ile	Pro	
			260					265					270			
Asn	Ile	Phe	Gln	Lys	Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg	
		275					280					285				
Met	Gly	Glu	Ser	Met	Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile	
	290					295					300					
Pro	Ile	Ile	Gly	Lys	Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser	
305					310					315					320	
Ile	Asp	Gln	Lys	Asn	Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser	
				325					330					335		
Gly	Phe	Glu	Pro	Pro	Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro	
			340					345					350			
Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu	
		355					360					365				
Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp	
	370					375					380					
Pro	Phe	Ile	Lys	Lys	Asn	Lys	Leu	Met	Ser	Leu	Leu	Thr	Ser	Pro	His	
385					390					395					400	
Gln	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Ser	Ala	Ser	Pro	Ser	Ala	Val	Pro	

## Cura 468 SEQ list 0405.txt

405

410

415

Asn	Gly	Pro	Gln	Ser	Pro	Lys	Gln	Gln	Lys	Glu	Pro	Leu	Ser	His	Arg
			420					425					430		
Phe	Asn	Glu	Phe	Met	Thr	Ser	Lys	Pro	Lys	Ile	His	Cys	Phe	Arg	Ser
		435					440					445			
Leu	Lys	Arg	Gly	Leu	Ser	Leu	Lys	Leu	Gly	Ala	Thr	Pro	Glu	Asp	Phe
	450					455					460				
Ser	Asn	Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Lys	Val
465					470					475					480
Asp	Glu	Leu	Asn	Lys	Glu	Ile	Gln	Lys	Glu	Met	Asp	Gln	Arg	Asp	Ala
				485					490					495	
Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn	Pro	Gln	Met	Gly	Asp
			500					505					510		
Pro	Ala	Ser	Leu	Asp	His	Lys	Leu	Ala	Glu	Val	Ser	Gln	Asn	Ile	Glu
		515					520					525			
Lys	Leu	Arg	Val	Glu	Thr	Gln	Lys	Phe	Glu	Ala	Trp	Leu	Ala	Glu	Val
	530					535					540				
Glu	Gly	Arg	Leu	Pro	Ala	Arg	Ser	Glu	Gln	Ala	Arg	Arg	Gln	Ser	Gly
545					550					555					560
Leu	Tyr	Asp	Ser	Gln	Asn	Pro	Pro	Thr	Val	Asn	Asn	Cys	Ala	Gln	Asp
				565					570					575	
Arg	Glu	Ser	Pro	Asp	Gly	Ser	Tyr	Thr	Glu	Glu	Gln	Ser	Gln	Glu	Ser
			580					585					590		
Glu	Met	Lys	Val	Leu	Ala	Thr	Asp	Phe	Asp	Asp	Glu	Phe	Asp	Asp	Glu
		595					600					605			
Glu	Pro	Leu	Pro	Ala	Ile	Gly	Thr	Cys	Lys	Ala	Leu	Tyr	Thr	Phe	Glu
	610					615					620				
Gly	Gln	Asn	Glu	Gly	Thr	Ile	Ser	Val	Val	Glu	Gly	Glu	Thr	Leu	Tyr
625					630					635					640
Val	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly	Trp	Thr	Arg	Ile	Arg	Arg	Asn
				645					650					655	
Glu	Asp	Glu	Glu	Gly	Tyr	Val	Pro	Thr	Ser	Tyr	Val	Glu	Val	Cys	Leu



660.

665

670

Asp Lys Asn Ala Lys Asp Ser  
675

&lt;210&gt; 70

&lt;211&gt; 674

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 70

Glu Glu Glu Pro Pro Arg Arg Pro Arg Ala Arg Ser Cys Glu Pro Glu  
1 5 10 15

Glu Ala Ala Arg Thr Pro Gly Phe Pro Pro Ser Arg Gly Ser Arg Gly  
20 25 30

Ala Lys Gly Ser Pro Gly Arg Gly Thr Arg Glu Pro Arg Pro Pro Arg  
35 40 45

Gly Ala Pro Leu Arg Val Pro Cys Thr Met Ser Trp Gly Thr Glu Leu  
50 55 60

Trp Asp Gln Phe Asp Asn Leu Glu Lys His Thr Gln Trp Gly Ile Asp  
65 70 75 80

Ile Leu Glu Lys Tyr Ile Lys Phe Val Lys Glu Arg Thr Glu Ile Glu  
85 90 95

Leu Ser Tyr Ala Lys Gln Leu Arg Asn Leu Ser Lys Lys Tyr Gln Pro  
100 105 110

Lys Lys Asn Ser Lys Glu Glu Glu Glu Tyr Lys Tyr Thr Ser Cys Lys  
115 120 125

Ala Phe Ile Ser Asn Leu Asn Glu Met Asn Asp Tyr Ala Gly Gln His  
130 135 140

Glu Val Ile Ser Glu Asn Met Ala Ser Gln Ile Ile Val Asp Leu Ala  
145 150 155 160

Arg Tyr Val Gln Glu Leu Lys Gln Glu Arg Lys Ser Asn Phe His Asp  
165 170 175

Gly Arg Lys Ala Gln Gln His Ile Glu Thr Cys Trp Lys Gln Leu Glu  
180 185 190

## Cura 468 SEQ list 0405.txt

Ser	Ser	Lys	Arg	Arg	Phe	Glu	Arg	Asp	Cys	Lys	Glu	Ala	Asp	Arg	Ala			
		195					200					205						
Gln	Gln	Tyr	Phe	Glu	Lys	Met	Asp	Ala	Asp	Ile	Asn	Val	Thr	Lys	Ala			
		210				215					220							
Asp	Val	Glu	Lys	Ala	Arg	Gln	Gln	Ala	Gln	Ile	Arg	His	Gln	Met	Ala			
225					230					235					240			
Glu	Asp	Ser	Lys	Ala	Asp	Tyr	Ser	Ser	Ile	Leu	Gln	Lys	Phe	Asn	His			
				245					250					255				
Glu	Gln	His	Glu	Tyr	Tyr	His	Thr	His	Ile	Pro	Asn	Ile	Phe	Gln	Lys			
			260					265					270					
Ile	Gln	Glu	Met	Glu	Glu	Arg	Arg	Ile	Val	Arg	Met	Gly	Glu	Ser	Met			
		275					280					285						
Lys	Thr	Tyr	Ala	Glu	Val	Asp	Arg	Gln	Val	Ile	Pro	Ile	Ile	Gly	Lys			
	290					295					300							
Cys	Leu	Asp	Gly	Ile	Val	Lys	Ala	Ala	Glu	Ser	Ile	Asp	Gln	Lys	Asn			
305					310					315					320			
Asp	Ser	Gln	Leu	Val	Ile	Glu	Ala	Tyr	Lys	Ser	Gly	Phe	Glu	Pro	Pro			
				325					330					335				
Gly	Asp	Ile	Glu	Phe	Glu	Asp	Tyr	Thr	Gln	Pro	Met	Lys	Arg	Thr	Val			
			340					345					350					
Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu	Gly	Lys	Pro	Asp	Leu			
		355					360					365						
Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp	Pro	Phe	Ile	Lys	Lys			
	370					375					380							
Asn	Lys	Leu	Met	Ser	Leu	Leu	Thr	Ser	Pro	His	Gln	Pro	Pro	Pro	Pro			
385					390					395					400			
Pro	Pro	Ala	Ser	Ala	Ser	Pro	Ser	Ala	Val	Pro	Asn	Gly	Pro	Gln	Ser			
				405					410					415				
Pro	Lys	Gln	Gln	Lys	Glu	Pro	Leu	Ser	His	Arg	Phe	Asn	Glu	Phe	Met			
			420					425					430					
Thr	Ser	Lys	Pro	Lys	Ile	His	Cys	Phe	Arg	Ser	Leu	Lys	Arg	Gly	Leu			
		435					440					445						

Cura 468 SEQ list 0405.txt

Ser	Leu	Lys	Leu	Gly	Ala	Thr	Pro	Glu	Asp	Phe	Ser	Asn	Leu	Pro	Pro
450						455					460				
Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Lys	Val	Asp	Glu	Leu	Asn	Lys
465					470					475					480
Glu	Ile	Gln	Lys	Glu	Met	Asp	Gln	Arg	Asp	Ala	Ile	Thr	Lys	Met	Lys
				485					490					495	
Asp	Val	Tyr	Leu	Lys	Asn	Pro	Gln	Met	Gly	Asp	Pro	Ala	Ser	Leu	Asp
			500					505					510		
His	Lys	Leu	Ala	Glu	Val	Ser	Gln	Asn	Ile	Glu	Lys	Leu	Arg	Val	Glu
		515					520					525			
Thr	Gln	Lys	Phe	Glu	Ala	Trp	Leu	Ala	Glu	Val	Glu	Gly	Arg	Leu	Pro
	530					535					540				
Ala	Arg	Ser	Glu	Gln	Ala	Arg	Arg	Gln	Ser	Gly	Leu	Tyr	Asp	Ser	Gln
545					550					555					560
Asn	Pro	Pro	Thr	Val	Asn	Asn	Cys	Ala	Gln	Asp	Arg	Glu	Ser	Pro	Asp
				565					570					575	
Gly	Ser	Tyr	Thr	Glu	Glu	Gln	Ser	Gln	Glu	Ser	Glu	Met	Lys	Val	Leu
			580					585					590		
Ala	Thr	Asp	Phe	Asp	Asp	Glu	Phe	Asp	Asp	Glu	Glu	Pro	Leu	Pro	Ala
		595					600					605			
Ile	Gly	Thr	Cys	Lys	Ala	Leu	Tyr	Thr	Phe	Glu	Gly	Gln	Asn	Glu	Gly
	610					615					620				
Thr	Ile	Ser	Val	Val	Glu	Gly	Glu	Thr	Leu	Tyr	Val	Ile	Glu	Glu	Asp
625					630					635					640
Lys	Gly	Asp	Gly	Trp	Thr	Arg	Ile	Arg	Arg	Asn	Glu	Asp	Glu	Glu	Gly
				645					650					655	
Tyr	Val	Pro	Thr	Ser	Tyr	Val	Glu	Val	Cys	Leu	Asp	Lys	Asn	Ala	Lys
			660					665					670		

Asp Ser

<210> 71  
<211> 457

## Cura 468 SEQ list 0405.txt

<212> PRT

<213> Homo sapiens

<400> 71

Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala  
1 5 10 15

Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln  
20 25 30

Gln His Pro Ile Ser Gln Ala Val Cys Trp Arg Ser Met Arg Arg Gly  
35 40 45

Cys Ala Val Leu Gly Ala Leu Gly Leu Leu Ala Gly Ala Gly Val Gly  
50 55 60

Ser Trp Leu Leu Val Leu Tyr Leu Cys Pro Ala Ala Ser Gln Pro Ile  
65 70 75 80

Ser Gly Thr Leu Gln Asp Glu Glu Ile Thr Leu Ser Cys Ser Glu Ala  
85 90 95

Ser Ala Glu Glu Ala Leu Leu Pro Ala Leu Pro Lys Thr Val Ser Phe  
100 105 110

Arg Ile Asn Ser Glu Asp Phe Leu Leu Glu Ala Gln Val Arg Asp Gln  
115 120 125

Pro Arg Trp Leu Leu Val Cys His Glu Gly Trp Ser Pro Ala Leu Gly  
130 135 140

Leu Gln Ile Cys Trp Ser Leu Gly His Leu Arg Leu Thr His His Lys  
145 150 155 160

Gly Val Asn Leu Thr Asp Ile Lys Leu Asn Ser Ser Gln Glu Phe Ala  
165 170 175

Gln Leu Ser Pro Arg Leu Gly Gly Phe Leu Glu Glu Ala Trp Gln Pro  
180 185 190

Arg Asn Asn Cys Thr Ser Gly Gln Val Val Ser Leu Arg Cys Ser Glu  
195 200 205

Cys Gly Ala Arg Pro Leu Ala Ser Arg Ile Val Gly Gly Gln Ser Val  
210 215 220

Ala Pro Gly Arg Trp Pro Trp Gln Ala Ser Val Ala Leu Gly Phe Arg  
225 230 235 240

Cura 468 SEQ list 0405.txt

His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala	Pro	Arg	Trp	Val	Val	Thr	Ala	
				245					250					255		
Ala	His	Cys	Met	His	Ser	Phe	Arg	Leu	Ala	Arg	Leu	Ser	Ser	Trp	Arg	
			260					265					270			
Val	His	Ala	Gly	Leu	Val	Ser	His	Ser	Ala	Val	Arg	Pro	His	Gln	Gly	
		275					280					285				
Ala	Leu	Val	Glu	Arg	Ile	Ile	Pro	His	Pro	Leu	Tyr	Ser	Ala	Gln	Asn	
	290					295					300					
His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Arg	Leu	Gln	Thr	Ala	Leu	Asn	Phe	
305					310					315				320		
Ser	Asp	Thr	Val	Gly	Ala	Val	Cys	Leu	Pro	Ala	Lys	Glu	Gln	His	Phe	
				325					330					335		
Pro	Lys	Gly	Ser	Arg	Cys	Trp	Val	Ser	Gly	Trp	Gly	His	Thr	His	Pro	
			340					345					350			
Ser	His	Thr	Tyr	Ser	Ser	Asp	Met	Leu	Gln	Asp	Thr	Val	Val	Pro	Leu	
		355					360					365				
Phe	Ser	Thr	Gln	Leu	Cys	Asn	Ser	Ser	Cys	Val	Tyr	Ser	Gly	Ala	Leu	
	370					375					380					
Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	Tyr	Leu	Asp	Gly	Arg	Ala	Asp	Ala	
385					390					395					400	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Pro	Asp	Gly	Asp	Thr	
				405					410					415		
Trp	Arg	Leu	Val	Gly	Val	Val	Ser	Trp	Gly	Arg	Ala	Cys	Ala	Glu	Pro	
			420					425					430			
Asn	His	Pro	Gly	Val	Tyr	Ala	Lys	Val	Ala	Glu	Phe	Leu	Asp	Trp	Ile	
		435					440					445				
His	Asp	Thr	Ala	Gln	Asp	Ser	Leu	Leu								
	450					455										

<210> 72

<211> 455

<212> PRT

<213> Mus musculus

Cura 468 SEQ list 0405.txt

<400> 72

Met	Ser	Pro	Thr	Leu	Asp	Asp	Gln	Ser	Pro	Met	Glu	Ile	Arg	Cys	Thr
1				5					10					15	
Glu	Glu	Gly	Ala	Gly	Pro	Gly	Ile	Phe	Arg	Met	Glu	Leu	Gly	Asp	Gln
			20					25					30		
Arg	Gln	Ser	Ile	Ser	Gln	Ser	Gln	Arg	Trp	Cys	Cys	Leu	Gln	Arg	Gly
		35					40					45			
Cys	Val	Ile	Leu	Gly	Val	Leu	Gly	Leu	Leu	Ala	Gly	Ala	Gly	Ile	Ala
	50					55					60				
Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Trp	Pro	Ala	Ala	Ser	Pro	Ser	Ile
65					70					75					80
Ser	Gly	Thr	Leu	Gln	Glu	Glu	Glu	Met	Thr	Leu	Asn	Cys	Pro	Gly	Val
				85					90					95	
Ser	Cys	Glu	Glu	Glu	Leu	Leu	Pro	Ser	Leu	Pro	Lys	Thr	Val	Ser	Phe
			100					105					110		
Arg	Ile	Asn	Gly	Glu	Asp	Leu	Leu	Leu	Gln	Val	Gln	Val	Arg	Ala	Arg
		115					120					125			
Pro	Asp	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly
	130					135					140				
Met	His	Ile	Cys	Lys	Ser	Leu	Gly	His	Ile	Arg	Leu	Thr	Gln	His	Lys
145					150					155					160
Ala	Val	Asn	Leu	Ser	Asp	Ile	Lys	Leu	Asn	Arg	Ser	Gln	Glu	Phe	Ala
				165					170					175	
Gln	Leu	Ser	Ala	Arg	Pro	Gly	Gly	Leu	Val	Glu	Glu	Ala	Trp	Lys	Pro
			180					185					190		
Ser	Ala	Asn	Cys	Pro	Ser	Gly	Arg	Ile	Val	Ser	Leu	Lys	Cys	Ser	Glu
		195					200					205			
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ala	Val
	210					215					220				
Ala	Ser	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Met	Leu	Gly	Ser	Arg
225					230					235					240
His	Thr	Cys	Gly	Ala	Ser	Val	Leu	Ala	Pro	His	Trp	Val	Val	Thr	Ala

## Cura 468 SEQ list 0405.txt

245

250

255

Ala	His	Cys	Met	Tyr	Ser	Phe	Arg	Leu	Ser	Arg	Leu	Ser	Ser	Trp	Arg
			260					265					270		
Val	His	Ala	Gly	Leu	Val	Ser	His	Gly	Ala	Val	Arg	Gln	His	Gln	Gly
		275					280					285			
Thr	Met	Val	Glu	Lys	Ile	Ile	Pro	His	Pro	Leu	Tyr	Ser	Ala	Gln	Asn
	290					295					300				
His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Gln	Leu	Arg	Thr	Pro	Ile	Asn	Phe
305					310					315					320
Ser	Asp	Thr	Val	Asp	Ala	Val	Cys	Leu	Pro	Ala	Lys	Glu	Gln	Tyr	Phe
				325					330					335	
Pro	Trp	Gly	Ser	Gln	Cys	Trp	Val	Ser	Gly	Trp	Gly	His	Thr	Asp	Pro
			340					345					350		
Ser	His	Thr	His	Ser	Ser	Asp	Thr	Leu	Gln	Asp	Thr	Met	Val	Pro	Leu
		355					360					365			
Leu	Ser	Thr	His	Leu	Cys	Asn	Ser	Ser	Cys	Met	Tyr	Ser	Gly	Ala	Leu
	370					375					380				
Thr	His	Arg	Met	Leu	Cys	Ala	Gly	Tyr	Leu	Asp	Gly	Arg	Ala	Asp	Ala
385					390					395					400
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Pro	Ser	Gly	Asp	Thr
				405					410					415	
Trp	His	Leu	Val	Gly	Val	Val	Ser	Trp	Gly	Arg	Gly	Cys	Ala	Glu	Pro
			420					425					430		
Asn	Arg	Pro	Gly	Val	Tyr	Ala	Lys	Val	Ala	Glu	Phe	Leu	Asp	Trp	Ile
		435					440					445			
His	Asp	Thr	Val	Gln	Val	Arg									
	450					455									

&lt;210&gt; 73

&lt;211&gt; 445

&lt;212&gt; PRT

&lt;213&gt; Mus musculus

&lt;400&gt; 73

## Cura 468 SEQ list 0405.txt

Met	Glu	Ile	Arg	Cys	Thr	Glu	Glu	Gly	Ala	Gly	Pro	Gly	Ile	Phe	Arg
1				5					10					15	
Met	Glu	Leu	Gly	Asp	Gln	Arg	Gln	Ser	Ile	Ser	Gln	Ser	Gln	Arg	Trp
			20					25					30		
Cys	Cys	Leu	Gln	Arg	Gly	Cys	Val	Ile	Leu	Gly	Val	Leu	Gly	Leu	Leu
		35					40					45			
Ala	Gly	Ala	Gly	Ile	Ala	Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Trp	Pro
	50					55					60				
Ala	Ala	Ser	Pro	Ser	Ile	Ser	Gly	Thr	Leu	Gln	Glu	Glu	Glu	Met	Thr
65					70					75					80
Leu	Asn	Cys	Pro	Gly	Val	Ser	Cys	Glu	Glu	Glu	Leu	Leu	Pro	Ser	Leu
				85					90					95	
Pro	Lys	Thr	Val	Ser	Phe	Arg	Ile	Asn	Gly	Glu	Asp	Leu	Leu	Leu	Gln
			100					105					110		
Val	Gln	Val	Arg	Ala	Arg	Pro	Asp	Trp	Leu	Leu	Val	Cys	His	Glu	Gly
		115					120					125			
Trp	Ser	Pro	Ala	Leu	Gly	Met	His	Ile	Cys	Lys	Ser	Leu	Gly	His	Ile
	130					135					140				
Arg	Leu	Thr	Gln	His	Lys	Ala	Val	Asn	Leu	Ser	Asp	Ile	Lys	Leu	Asn
145					150					155					160
Arg	Ser	Gln	Glu	Phe	Ala	Gln	Leu	Ser	Ala	Arg	Pro	Gly	Gly	Leu	Val
				165					170					175	
Glu	Glu	Ala	Trp	Lys	Pro	Ser	Ala	Asn	Cys	Pro	Ser	Gly	Arg	Ile	Val
			180					185					190		
Ser	Leu	Lys	Cys	Ser	Glu	Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile
		195					200					205			
Val	Gly	Gly	Gln	Ala	Val	Ala	Ser	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser
	210					215					220				
Val	Met	Leu	Gly	Ser	Arg	His	Thr	Cys	Gly	Ala	Ser	Val	Leu	Ala	Pro
225					230					235					240
His	Trp	Val	Val	Thr	Ala	Ala	His	Cys	Met	Tyr	Ser	Phe	Arg	Leu	Ser
				245					250					255	



Cura 468 SEQ list 0405.txt

Arg Leu Ser Ser Trp Arg Val His Ala Gly Leu Val Ser His Gly Ala  
260 265 270

Val Arg Gln His Gln Gly Thr Met Val Glu Lys Ile Ile Pro His Pro  
275 280 285

Leu Tyr Ser Ala Gln Asn His Asp Tyr Asp Val Ala Leu Leu Gln Leu  
290 295 300

Arg Thr Pro Ile Asn Phe Ser Asp Thr Val Gly Ala Val Cys Leu Pro  
305 310 315 320

Ala Lys Glu Gln Tyr Phe Pro Trp Gly Ser Gln Cys Trp Val Ser Gly  
325 330 335

Trp Gly His Thr Asp Pro Ser His Thr His Ser Ser Asp Thr Leu Gln  
340 345 350

Asp Thr Met Val Pro Leu Leu Ser Thr His Leu Cys Asn Ser Ser Cys  
355 360 365

Met Tyr Ser Gly Ala Leu Thr His Arg Met Leu Cys Ala Gly Tyr Leu  
370 375 380

Asp Gly Arg Ala Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val  
385 390 395 400

Cys Pro Ser Gly Asp Thr Trp His Leu Val Gly Val Val Ser Trp Gly  
405 410 415

Arg Gly Cys Ala Glu Pro Asn Arg Pro Gly Val Tyr Ala Lys Val Ala  
420 425 430

Glu Phe Leu Asp Trp Ile His Asp Thr Val Gln Val Arg  
435 440 445

<210> 74

<211> 398

<212> PRT

<213> Homo sapiens

<400> 74

Met Ser Leu Met Leu Asp Asp Gln Pro Pro Met Glu Ala Gln Tyr Ala  
1 5 10 15

Glu Glu Gly Pro Gly Pro Gly Ile Phe Arg Ala Glu Pro Gly Asp Gln  
20 25 30

Cura 468 SEQ list 0405.txt

Gln	His	Pro	Ile	Ser	Gln	Ala	Val	Cys	Trp	Arg	Ser	Met	Arg	Arg	Gly
		35					40					45			
Cys	Ala	Val	Leu	Gly	Ala	Leu	Gly	Leu	Leu	Ala	Gly	Ala	Gly	Val	Gly
	50					55					60				
Ser	Trp	Leu	Leu	Val	Leu	Tyr	Leu	Cys	Pro	Ala	Ala	Ser	Gln	Pro	Ile
65					70					75					80
Ser	Gly	Thr	Leu	Gln	Asp	Glu	Glu	Ile	Thr	Leu	Ser	Cys	Ser	Glu	Ala
				85					90					95	
Ser	Ala	Glu	Glu	Ala	Leu	Leu	Pro	Ala	Leu	Pro	Lys	Thr	Val	Ser	Phe
			100					105					110		
Arg	Ile	Asn	Ser	Glu	Asp	Phe	Leu	Leu	Glu	Ala	Gln	Val	Arg	Asp	Gln
		115					120					125			
Pro	Arg	Trp	Leu	Leu	Val	Cys	His	Glu	Gly	Trp	Ser	Pro	Ala	Leu	Gly
	130					135					140				
Leu	Gln	Ile	Cys	Trp	Ser	Leu	Gly	His	Leu	Arg	Leu	Thr	His	His	Lys
145					150					155					160
Gly	Val	Asn	Leu	Thr	Asp	Ile	Lys	Leu	Asn	Ser	Ser	Gln	Glu	Phe	Ala
				165					170					175	
Gln	Leu	Ser	Pro	Arg	Leu	Gly	Gly	Phe	Leu	Glu	Glu	Ala	Trp	Gln	Pro
			180					185					190		
Arg	Asn	Asn	Cys	Thr	Ser	Gly	Gln	Val	Val	Ser	Leu	Arg	Cys	Ser	Glu
		195					200					205			
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ser	Val
	210					215					220				
Ala	Pro	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Ala	Leu	Gly	Phe	Arg
225					230					235					240
His	Thr	Cys	Gly	Gly	Ser	Val	Leu	Ala	Pro	Arg	Trp	Val	Val	Thr	Ala
				245					250					255	
Ala	His	Cys	Met	His	Ser	Phe	Arg	Leu	Ala	Arg	Leu	Ser	Ser	Trp	Arg
			260					265					270		
Val	His	Ala	Gly	Leu	Val	Ser	His	Ser	Ala	Val	Arg	Pro	His	Gln	Gly
		275					280					285			

Cura 468 SEQ list 0405.txt

Ala	Leu	Val	Glu	Arg	Ile	Ile	Pro	His	Pro	Leu	Tyr	Ser	Ala	Gln	Asn
290						295					300				
His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Arg	Leu	Gln	Thr	Ala	Leu	Asn	Phe
305					310					315					320
Ser	Asp	Thr	Val	Gly	Ala	Val	Cys	Leu	Pro	Ala	Lys	Glu	Gln	His	Phe
				325					330					335	
Pro	Lys	Gly	Ser	Arg	Cys	Trp	Val	Ser	Gly	Trp	Gly	His	Thr	His	Pro
			340					345					350		
Ser	His	Ser	Leu	Gln	Leu	Gly	Tyr	Ala	Pro	Gly	His	Gly	Gly	Ala	Leu
		355					360					365			
Val	Gln	His	Ser	Ala	Leu	Gln	Gln	Leu	Leu	Arg	Val	Gln	Arg	Ser	Pro
	370					375					380				
His	Pro	Pro	His	Ala	Leu	Arg	Trp	Leu	Pro	Gly	Arg	Lys	Gly		
385					390					395					

<210> 75  
 <211> 311  
 <212> PRT  
 <213> Mus musculus

<400> 75

Met	His	Ile	Cys	Lys	Ser	Leu	Gly	His	Ile	Arg	Leu	Thr	Gln	His	Lys
1				5					10					15	
Ala	Val	Asn	Leu	Ser	Asp	Ile	Lys	Leu	Asn	Arg	Ser	Gln	Glu	Phe	Ala
			20					25					30		
Gln	Leu	Ser	Ala	Arg	Pro	Gly	Gly	Leu	Val	Glu	Glu	Ala	Trp	Lys	Pro
		35					40					45			
Ser	Ala	Asn	Cys	Pro	Ser	Gly	Arg	Ile	Val	Ser	Leu	Lys	Cys	Ser	Glu
	50					55					60				
Cys	Gly	Ala	Arg	Pro	Leu	Ala	Ser	Arg	Ile	Val	Gly	Gly	Gln	Ala	Val
65					70					75					80
Ala	Ser	Gly	Arg	Trp	Pro	Trp	Gln	Ala	Ser	Val	Met	Leu	Gly	Ser	Arg
				85					90					95	
His	Thr	Cys	Gly	Ala	Ser	Val	Leu	Ala	Pro	His	Trp	Val	Val	Thr	Ala

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100					105					110					
Ala	His	Cys	Met	Tyr	Ser	Phe	Arg	Leu	Ser	Arg	Leu	Ser	Ser	Trp	Arg
		115				.	120					125			
Val	His	Ala	Gly	Leu	Val	Ser	His	Gly	Ala	Val	Arg	Gln	His	Gln	Gly
	130					135					140				
Thr	Met	Val	Glu	Lys	Ile	Ile	Pro	His	Pro	Leu	Tyr	Ser	Ala	Gln	Asn
145					150					155					160
His	Asp	Tyr	Asp	Val	Ala	Leu	Leu	Gln	Leu	Arg	Thr	Pro	Ile	Asn	Phe
				165					170					175	
Ser	Asp	Thr	Val	Asp	Ala	Val	Cys	Leu	Pro	Ala	Lys	Glu	Gln	Tyr	Phe
			180					185					190		
Pro	Trp	Gly	Ser	Gln	Cys	Trp	Val	Ser	Gly	Trp	Gly	His	Thr	Asp	Pro
		195					200					205			
Ser	His	Thr	His	Ser	Ser	Asp	Thr	Leu	Gln	Asp	Thr	Met	Val	Pro	Leu
	210					215					220				
Leu	Ser	Thr	His	Leu	Cys	Asn	Ser	Ser	Cys	Met	Tyr	Ser	Gly	Ala	Leu
225					230					235					240
Thr	His	Arg	Met	Leu	Cys	Ala	Gly	Tyr	Leu	Asp	Gly	Arg	Ala	Asp	Ala
				245					250					255	
Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Pro	Ser	Gly	Asp	Thr
			260					265					270		
Trp	His	Leu	Val	Gly	Val	Val	Ser	Trp	Gly	Arg	Gly	Cys	Ala	Glu	Pro
		275					280					285			
Asn	Arg	Pro	Gly	Val	Tyr	Ala	Lys	Val	Ala	Glu	Phe	Leu	Asp	Trp	Ile
	290					295					300				
His	Asp	Thr	Val	Gln	Val	Arg									
305					310										

&lt;210&gt; 76

&lt;211&gt; 199

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Reprolysin  
family zinc protease Consensus Sequence

&lt;400&gt; 76

Lys	Tyr	Ile	Glu	Leu	Phe	Ile	Val	Val	Asp	His	Gly	Met	Phe	Thr	Lys
1				5					10					15	

Tyr	Gly	Ser	Asp	Leu	Asn	Lys	Ile	Arg	Gln	Arg	Val	His	Gln	Ile	Val
			20					25					30		

Asn	Leu	Val	Asn	Glu	Ile	Tyr	Arg	Pro	Leu	Asn	Ile	Arg	Val	Val	Leu
		35					40					45			

Val	Gly	Leu	Glu	Ile	Trp	Ser	Asp	Gly	Asp	Lys	Ile	Thr	Val	Gln	Gly
	50					55					60				

Asp	Ala	Asn	Asp	Thr	Leu	His	Arg	Phe	Leu	Glu	Trp	Arg	Glu	Thr	Asp
65					70					75					80

Leu	Leu	Lys	Arg	Lys	Ser	His	Asp	Asn	Ala	Gln	Leu	Leu	Thr	Gly	Ile
				85					90					95	

Asp	Phe	Asp	Gly	Asn	Thr	Ile	Gly	Ala	Ala	Tyr	Val	Gly	Gly	Met	Cys
			100					105					110		

Ser	Pro	Lys	Arg	Ser	Val	Gly	Val	Val	Gln	Asp	His	Ser	Pro	Ile	Val
		115					120					125			

Leu	Leu	Val	Ala	Val	Thr	Met	Ala	His	Glu	Leu	Gly	His	Asn	Leu	Gly
		130				135					140				

Met	Thr	His	Asp	Asp	Ile	Asn	Lys	Cys	Thr	Cys	Glu	Gly	Gly	Gly	Gly
145					150					155					160

Cys	Ile	Met	Asn	Pro	Val	Ala	Ser	Ser	Ser	Pro	Gly	Lys	Lys	Phe	Ser
				165					170					175	

Asn	Cys	Ser	Met	Asp	Asp	Tyr	Gln	Gln	Phe	Leu	Thr	Lys	Gly	Lys	Pro
			180					185					190		

Gln	Cys	Leu	Leu	Asn	Lys	Pro
		195				

&lt;210&gt; 77

&lt;211&gt; 51

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thrombospondin  
type 1 Consensus Sequence

<400> 77

Trp Gly Glu Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Gly  
1 5 10 15

Gly Val Gln Thr Arg Thr Arg Cys Cys Asn Pro Pro Pro Asn Gly Gly  
20 25 30

Gly Pro Cys Thr Gly Pro Asp Thr Glu Thr Arg Ala Cys Asn Glu Gln  
35 40 45

Pro Cys Pro  
50

<210> 78

<211> 48

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Thrombospondin  
type 1 domain Consensus Sequence

<400> 78

Ser Pro Trp Ser Glu Trp Ser Pro Cys Ser Val Thr Cys Gly Lys Gly  
1 5 10 15

Ile Arg Thr Arg Gln Arg Thr Cys Asn Ser Pro Ala Gly Gly Lys Pro  
20 25 30

Cys Thr Gly Asp Ala Gln Glu Thr Glu Ala Cys Met Met Asp Pro Cys  
35 40 45

<210> 79

<211> 117

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Reprolysin  
family propeptide Consensus Sequence

<400> 79

His	Leu	Glu	Lys	Asn	Arg	Ser	Leu	Leu	Ala	Pro	Asp	Phe	Thr	Val	Thr
1				5					10					15	
Thr	Tyr	Asp	Asp	Asp	Gly	Thr	Leu	Val	Thr	Glu	His	Pro	Leu	Ile	Gln
			20					25					30		
Asp	His	Cys	Tyr	Tyr	Gln	Gly	Tyr	Val	Glu	Gly	Tyr	Pro	Asn	Ser	Ala
		35					40					45			
Val	Ser	Leu	Ser	Thr	Cys	Ser	Gly	Leu	Arg	Gly	Ile	Leu	Gln	Leu	Glu
	50					55					60				
Asn	Leu	Ser	Tyr	Gly	Ile	Glu	Pro	Leu	Glu	Ser	Ser	Asp	Gly	Phe	Glu
65					70					75					80
His	Ile	Ile	Tyr	Gln	Ile	Glu	His	Leu	Lys	Thr	Val	Pro	Gly	Pro	Cys
				85					90					95	
Gly	Glu	Cys	Gly	Ser	Leu	Ser	Val	Ser	Thr	Asp	Ser	Gln	Tyr	Gly	Ile
			100					105					110		
Arg	Ser	Pro	Ser	Pro											
			115												

<210> 80

<211> 751

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
Alpha-2-macroglobulin family Consensus Sequence

<400> 80

Ile	Asp	Glu	Asp	Asp	Ile	Thr	Ile	Arg	Ser	Tyr	Phe	Pro	Glu	Ser	Trp
1				5					10					15	
Leu	Trp	Glu	Val	Glu	Glu	Val	Asp	Arg	Ser	Pro	Val	Leu	Thr	Val	Asn
			20					25					30		
Ile	Thr	Leu	Pro	Asp	Ser	Ile	Thr	Thr	Trp	Glu	Ile	Leu	Ala	Val	Ser
		35					40					45			

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Leu	Ser	Asn	Thr	Lys	Gly	Leu	Cys	Val	Ala	Asp	Pro	Val	Glu	Leu	Thr
50						55					60				
Val	Phe	Gln	Asp	Phe	Phe	Leu	Glu	Leu	Arg	Leu	Pro	Tyr	Ser	Val	Val
65					70					75					80
Arg	Gly	Glu	Gln	Val	Glu	Leu	Arg	Ala	Val	Leu	Tyr	Asn	Tyr	Leu	Pro
				85					90					95	
Ser	Gln	Asp	Ile	Lys	Val	Val	Val	Gln	Leu	Glu	Val	Glu	Pro	Leu	Cys
			100					105					110		
Gln	Ala	Gly	Phe	Cys	Ser	Leu	Ala	Thr	Gln	Arg	Thr	Arg	Ser	Ser	Gln
		115					120					125			
Ser	Val	Arg	Pro	Lys	Ser	Leu	Ser	Ser	Val	Ser	Phe	Pro	Val	Val	Val
	130					135					140				
Val	Pro	Leu	Ala	Ser	Gly	Leu	Ser	Leu	Val	Glu	Val	Val	Ala	Ser	Val
145					150					155					160
Pro	Glu	Phe	Phe	Val	Lys	Asp	Ala	Val	Val	Lys	Thr	Leu	Lys	Val	Glu
				165					170					175	
Pro	Glu	Gly	Ala	Arg	Lys	Glu	Glu	Thr	Val	Ser	Ser	Leu	Leu	Leu	Pro
			180					185					190		
Pro	Glu	His	Leu	Gly	Gly	Gly	Leu	Glu	Val	Ser	Glu	Val	Pro	Ala	Leu
		195					200					205			
Lys	Leu	Pro	Asp	Asp	Val	Pro	Asp	Thr	Glu	Ala	Glu	Ala	Val	Ile	Ser
	210					215					220				
Val	Gln	Gly	Asp	Pro	Val	Ala	Gln	Ala	Ile	Gln	Asn	Thr	Leu	Ser	Gly
225					230					235					240
Glu	Gly	Leu	Asn	Asn	Leu	Leu	Arg	Leu	Pro	Ser	Gly	Cys	Gly	Glu	Gln
				245					250					255	
Asn	Met	Ile	Tyr	Met	Ala	Pro	Thr	Val	Tyr	Val	Leu	His	Tyr	Leu	Asp
			260					265					270		
Glu	Thr	Trp	Gln	Trp	Glu	Lys	Pro	Gly	Thr	Lys	Lys	Lys	Gln	Lys	Ala
		275					280					285			
Ile	Asp	Leu	Ile	Asn	Lys	Gly	Tyr	Gln	Arg	Gln	Leu	Asn	Tyr	Arg	Lys
	290					295					300				



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Ala	Asp	Gly	Ser	Tyr	Ala	Ala	Phe	Leu	His	Arg	Ala	Ser	Ser	Thr	Trp
305					310					315					320
Leu	Thr	Ala	Phe	Val	Leu	Lys	Val	Phe	Ser	Gln	Ala	Arg	Asn	Tyr	Val
				325					330					335	
Phe	Ile	Asp	Glu	Glu	His	Ile	Cys	Gly	Ala	Val	Lys	Trp	Leu	Ile	Leu
			340					345					350		
Asn	Gln	Gln	Lys	Asp	Asp	Gly	Val	Phe	Arg	Glu	Ser	Gly	Pro	Val	Ile
		355					360					365			
His	Asn	Glu	Met	Lys	Gly	Gly	Val	Gly	Asp	Asp	Ala	Glu	Val	Glu	Val
	370					375					380				
Thr	Leu	Thr	Ala	Phe	Ile	Thr	Ile	Ala	Leu	Leu	Glu	Ala	Lys	Leu	Val
385					390					395					400
Cys	Ile	Ser	Pro	Val	Val	Ala	Asn	Ala	Leu	Ser	Ile	Leu	Lys	Ala	Ser
				405					410					415	
Asp	Tyr	Leu	Leu	Glu	Asn	Tyr	Ala	Asn	Gly	Gln	Arg	Val	Tyr	Thr	Leu
			420					425					430		
Ala	Leu	Thr	Ala	Tyr	Ala	Leu	Ala	Leu	Ala	Gly	Val	Leu	His	Lys	Leu
		435					440					445			
Lys	Glu	Ile	Leu	Lys	Ser	Leu	Lys	Glu	Glu	Leu	Tyr	Lys	Ala	Leu	Val
	450					455					460				
Lys	Gly	His	Trp	Glu	Arg	Pro	Gln	Lys	Pro	Lys	Asp	Ala	Pro	Gly	His
465					470					475					480
Pro	Tyr	Ser	Pro	Gln	Pro	Gln	Ala	Ala	Ala	Val	Glu	Met	Thr	Ser	Tyr
				485					490					495	
Ala	Leu	Leu	Ala	Leu	Leu	Thr	Leu	Leu	Pro	Phe	Pro	Lys	Val	Glu	Met
			500					505					510		
Ala	Pro	Lys	Val	Val	Lys	Trp	Leu	Thr	Glu	Gln	Gln	Tyr	Tyr	Gly	Gly
		515					520					525			
Gly	Phe	Gly	Ser	Thr	Gln	Asp	Thr	Val	Met	Ala	Leu	Gln	Ala	Leu	Ser
	530					535					540				
Lys	Tyr	Gly	Ile	Ala	Thr	Pro	Thr	His	Lys	Glu	Lys	Asn	Leu	Ser	Val
545					550					555					560

Cura 468 SEQ list 0405.txt

Thr	Ile	Gln	Ser	Pro	Ser	Gly	Ser	Phe	Lys	Ser	His	Phe	Gln	Ile	Leu
				565					570					575	
Asn	Asn	Asn	Ala	Phe	Leu	Leu	Arg	Pro	Val	Glu	Leu	Pro	Leu	Asn	Glu
			580					585					590		
Gly	Phe	Thr	Val	Thr	Ala	Lys	Val	Thr	Gly	Gln	Gly	Thr	Leu	Thr	Leu
		595					600					605			
Val	Thr	Thr	Tyr	Arg	Tyr	Lys	Val	Leu	Asp	Lys	Lys	Asn	Thr	Phe	Cys
	610					615					620				
Phe	Asp	Leu	Lys	Ile	Glu	Thr	Val	Pro	Asp	Thr	Cys	Val	Glu	Pro	Lys
625					630					635					640
Gly	Ala	Lys	Asn	Ser	Asp	Tyr	Leu	Ser	Ile	Cys	Thr	Arg	Tyr	Ala	Gly
			645						650					655	
Ser	Arg	Ser	Asp	Ser	Gly	Met	Ala	Ile	Ala	Asp	Ile	Ser	Met	Leu	Thr
			660					665					670		
Gly	Phe	Ile	Pro	Leu	Lys	Pro	Asp	Leu	Lys	Lys	Leu	Glu	Asn	Gly	Val
		675					680					685			
Asp	Arg	Tyr	Val	Ser	Lys	Tyr	Glu	Ile	Asp	Gly	Asn	His	Val	Leu	Leu
	690					695					700				
Tyr	Leu	Asp	Lys	Val	Ser	His	Ser	Glu	Thr	Glu	Cys	Val	Gly	Phe	Lys
705					710					715					720
Ile	His	Gln	Asp	Phe	Glu	Val	Gly	Leu	Leu	Gln	Pro	Ala	Ser	Val	Lys
			725						730					735	
Val	Tyr	Asp	Tyr	Tyr	Glu	Pro	Asp	Glu	Gln	Cys	Thr	Ala	Phe	Tyr	
			740					745					750		

<210> 81

<211> 620

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Alpha-2-macroglobulin family N-terminal region  
Consensus Sequence

<400> 81

## Cura 468 SEQ list 0405.txt

Arg	Leu	Leu	Trp	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Phe	Phe	Asp	Ser	Ser
1				5					10					15	
Leu	Gln	Lys	Pro	Arg	Tyr	Met	Val	Ile	Val	Pro	Ser	Ile	Leu	Arg	Thr
			20					25					30		
Glu	Thr	Pro	Glu	Lys	Val	Cys	Val	Gln	Leu	His	Asp	Leu	Asn	Glu	Thr
		35					40					45			
Val	Thr	Val	Thr	Val	Ser	Leu	His	Ser	Phe	Pro	Gly	Lys	Arg	Asn	Leu
	50					55					60				
Ser	Ser	Leu	Phe	Thr	Val	Leu	Leu	Ser	Ser	Lys	Asp	Leu	Phe	His	Cys
65					70					75					80
Val	Ser	Phe	Thr	Val	Pro	Gln	Pro	Gly	Leu	Phe	Lys	Ser	Ser	Lys	Gly
				85					90					95	
Glu	Glu	Ser	Phe	Val	Val	Val	Gln	Val	Lys	Gly	Pro	Thr	His	Thr	Phe
			100					105					110		
Lys	Glu	Lys	Val	Thr	Val	Leu	Val	Ser	Ser	Arg	Arg	Gly	Leu	Val	Phe
		115					120					125			
Ile	Gln	Thr	Asp	Lys	Pro	Ile	Tyr	Thr	Pro	Gly	Gln	Thr	Val	Arg	Tyr
	130					135					140				
Arg	Val	Phe	Ser	Val	Asp	Glu	Asn	Leu	Arg	Pro	Leu	Asn	Glu	Leu	Ile
145					150					155					160
Leu	Val	Tyr	Ile	Glu	Asp	Pro	Glu	Gly	Asn	Arg	Val	Asp	Gln	Trp	Glu
				165					170					175	
Val	Asn	Lys	Leu	Glu	Gly	Gly	Ile	Phe	Gln	Leu	Ser	Phe	Pro	Ile	Pro
			180					185					190		
Ser	Glu	Pro	Ile	Gln	Gly	Thr	Trp	Lys	Ile	Val	Ala	Arg	Tyr	Glu	Ser
		195					200					205			
Gly	Pro	Glu	Ser	Asn	Tyr	Thr	His	Tyr	Phe	Glu	Val	Lys	Glu	Tyr	Val
	210					215					220				
Leu	Pro	Ser	Phe	Glu	Val	Ser	Ile	Thr	Pro	Pro	Lys	Pro	Phe	Ile	Tyr
225					230					235					240
Tyr	Asp	Asn	Phe	Lys	Glu	Phe	Glu	Val	Thr	Ile	Cys	Ala	Arg	Tyr	Thr
				245					250					255	

## Cura 468 SEQ list 0405.txt

Tyr	Gly	Lys	Pro	Val	Pro	Gly	Val	Ala	Tyr	Val	Arg	Phe	Gly	Val	Lys	260	265	270
Asp	Glu	Asp	Gly	Lys	Lys	Glu	Leu	Leu	Ala	Gly	Leu	Glu	Glu	Arg	Ala	275	280	285
Lys	Leu	Leu	Asp	Gly	Asn	Gly	Glu	Ile	Cys	Leu	Ser	Gln	Glu	Val	Leu	290	295	300
Leu	Lys	Glu	Leu	Gln	Leu	Lys	Asn	Glu	Asp	Leu	Glu	Gly	Lys	Ser	Leu	305	310	315
Tyr	Val	Ala	Val	Ala	Val	Ile	Glu	Ser	Glu	Gly	Gly	Asp	Met	Glu	Glu	325	330	335
Ala	Glu	Leu	Gly	Gly	Ile	Lys	Ile	Val	Arg	Ser	Pro	Tyr	Lys	Leu	Lys	340	345	350
Phe	Val	Lys	Thr	Pro	Ser	His	Phe	Lys	Pro	Gly	Ile	Pro	Phe	Phe	Leu	355	360	365
Lys	Val	Leu	Val	Val	Asp	Pro	Asp	Gly	Ser	Pro	Ala	Pro	Asn	Val	Pro	370	375	380
Val	Lys	Val	Ser	Ala	Gln	Asp	Ala	Ser	Tyr	Tyr	Ser	Asn	Gly	Thr	Thr	385	390	395
Asp	Glu	Asp	Gly	Leu	Ala	Gln	Phe	Ser	Ile	Asn	Thr	Ser	Gly	Ile	Ser	405	410	415
Ser	Leu	Ser	Ile	Thr	Val	Arg	Thr	Asn	His	Lys	Glu	Leu	Pro	Glu	Glu	420	425	430
Val	Gln	Ala	His	Ala	Glu	Ala	Gln	Ala	Thr	Ala	Tyr	Ser	Thr	Val	Ser	435	440	445
Leu	Ser	Lys	Ser	Tyr	Ile	His	Leu	Ser	Ile	Glu	Arg	Thr	Leu	Pro	Cys	450	455	460
Gly	Pro	Gly	Val	Gly	Glu	Gln	Ala	Asn	Phe	Ile	Leu	Arg	Gly	Lys	Ser	465	470	475
Leu	Gly	Glu	Leu	Lys	Ile	Leu	His	Phe	Tyr	Tyr	Leu	Ile	Met	Ser	Lys	485	490	495
Gly	Lys	Ile	Val	Lys	Thr	Gly	Arg	Glu	Pro	Arg	Glu	Pro	Gly	Gln	Gly	500	505	510

Cura 468 SEQ list 0405.txt

Leu Phe Ser Leu Ser Ile Pro Val Thr Pro Asp Leu Ala Pro Ser Phe  
515 520 525

Arg Leu Val Ala Tyr Tyr Ile Leu Pro Gln Gly Glu Val Val Ala Asp  
530 535 540

Ser Val Trp Ile Asp Val Glu Asp Cys Cys Ala Asn Lys Leu Asp Leu  
545 550 555 560

Ser Phe Ser Pro Ser Lys Asp Tyr Arg Leu Pro Ala Gln Gln Val Lys  
565 570 575

Leu Arg Val Glu Ala Asp Pro Gln Ser Leu Val Ala Leu Arg Ala Val  
580 585 590

Asp Gln Ala Val Tyr Leu Leu Lys Pro Lys Ala Lys Leu Ser Met Ser  
595 600 605

Lys Val Tyr Asp Leu Leu Glu Lys Ser Asp Leu Gly  
610 615 620

<210> 82

<211> 186

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Sodium Bile  
acid symporter family consensus sequence

<400> 82

Ala Leu Gly Leu Phe Leu Met Met Phe Ser Met Gly Leu Lys Val Arg  
1 5 10 15

Phe Glu Asp Leu Lys Glu Ala Leu Arg Arg Pro Lys Ala Leu Ile Leu  
20 25 30

Gly Leu Leu Leu Gln Trp Ile Ile Met Pro Leu Leu Met Phe Ile Leu  
35 40 45

Ala Trp Leu Leu Leu Arg Leu Pro Pro Glu Leu Ala Thr Gly Leu Ile  
50 55 60

Leu Val Gly Cys Ala Pro Gly Gly Ala Met Ser Asn Val Trp Thr Tyr  
65 70 75 80

Leu Ala Lys Gly Asp Val Glu Leu Ser Val Val Met Val Ala Leu Ser

## Cura 468 SEQ list 0405.txt

85

90

95

Thr Leu Leu Ala Pro Leu Val Thr Pro Leu Leu Ser Phe Leu Leu Ala  
 100 105 110

Gly Leu Leu Val His Val Asp Ala Val Ser Pro Trp Ser Leu Ile Lys  
 115 120 125

Ser Val Leu Val Tyr Val Ile Ile Pro Leu Ile Ala Gly Met Leu Thr  
 130 135 140

Arg Tyr Phe Leu Pro Glu Trp Phe Glu Gln Arg Val Leu Pro Val Leu  
 145 150 155 160

Ser Pro Ile Ser Leu Ile Gly Leu Leu Leu Thr Ile Val Val Ile Phe  
 165 170 175

Ala Leu Asn Gly Glu Val Ile Ala Ser Leu  
 180 185

&lt;210&gt; 83

&lt;211&gt; 191

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: SPFH  
 domain/Band 7 family Consensus Sequence

&lt;400&gt; 83

Val Ala Leu Leu Ile Ile Ile Ala Leu Val Val Ile Ala Met Ser Val  
 1 5 10 15

Lys Ile Val Lys Glu Tyr Glu Arg Gly Val Ile Phe Arg Leu Gly Arg  
 20 25 30

Tyr Val Arg Gln Val Val Gly Pro Gly Leu His Phe Ile Ile Pro Phe  
 35 40 45

Ile Asp Thr Val Lys Lys Val Asp Leu Arg Thr Val Val Tyr Asp Val  
 50 55 60

Pro Ser Gln Glu Ile Ile Thr Lys Asp Asn Val Val Val Ile Val Asp  
 65 70 75 80

Ala Val Val Tyr Tyr Arg Val Val Asp Pro Leu Lys Ala Val Tyr Glu  
 85 90 95

Cura 468 SEQ list 0405.txt

Val	Glu	Asp	Ala	Glu	Arg	Ala	Leu	Pro	Gln	Leu	Ala	Gln	Thr	Thr	Leu
			100					105					110		
Arg	Asn	Val	Ile	Gly	Gln	Phe	Thr	Leu	Asp	Glu	Ile	Leu	Thr	Glu	Arg
		115					120					125			
Glu	Arg	Ile	Asn	Ser	Gln	Leu	Arg	Glu	Ile	Leu	Asp	Glu	Ala	Thr	Asp
		130				135					140				
Pro	Trp	Gly	Ile	Lys	Val	Glu	Arg	Val	Glu	Ile	Lys	Asp	Ile	Arg	Leu
145					150					155					160
Pro	Glu	Glu	Val	Gln	Arg	Ala	Met	Ala	Ala	Gln	Met	Glu	Ala	Glu	Arg
				165					170					175	
Glu	Ala	Arg	Ala	Lys	Ile	Leu	Glu	Ala	Glu	Gly	Glu	Gln	Glu	Ala	
			180					185					190		

<210> 84

<211> 160

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Prohibitin  
homologues Consensus Sequence

<400> 84

Ala	Ala	Phe	Tyr	Val	Ile	Gly	Glu	Gly	Glu	Arg	Gly	Val	Val	Glu	Arg
1				5					10					15	
Leu	Gly	Arg	Val	Leu	Lys	Val	Leu	Gly	Pro	Gly	Leu	His	Phe	Val	Ile
			20					25					30		
Pro	Phe	Ile	Asp	Asp	Val	Lys	Arg	Val	Asp	Leu	Arg	Ala	Gln	Thr	Asp
			35				40					45			
Asp	Val	Pro	Pro	Gln	Glu	Val	Ile	Thr	Lys	Asp	Asn	Val	Thr	Val	Ser
		50				55					60				
Val	Asp	Ala	Val	Val	Tyr	Tyr	Arg	Val	Leu	Asp	Pro	Leu	Lys	Ala	Val
65					70					75					80
Tyr	Gly	Val	Leu	Asp	Ala	Asp	Tyr	Arg	Ala	Leu	Arg	Gln	Leu	Ala	Gln
				85					90					95	

Cura 468 SEQ list 0405.txt

Thr	Thr	Leu	Arg	Ser	Val	Ile	Gly	Lys	Arg	Thr	Leu	Asp	Glu	Leu	Leu
			100					105					110		
Thr	Asp	Glu	Arg	Glu	Lys	Ile	Ser	Glu	Asn	Ile	Arg	Glu	Glu	Leu	Asn
		115					120					125			
Glu	Ala	Ala	Glu	Pro	Trp	Gly	Ile	Glu	Val	Glu	Asp	Val	Glu	Ile	Lys
	130					135					140				
Asp	Ile	Arg	Leu	Pro	Glu	Glu	Ile	Lys	Glu	Ala	Met	Glu	Ala	Gln	Gln
145					150					155					160

<210> 85  
 <211> 79  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Kringle domain  
 Consensus Sequence

<400> 85															
Cys	Tyr	His	Gly	Asn	Gly	Glu	Asn	Tyr	Arg	Gly	Thr	Ala	Ser	Thr	Thr
1				5					10					15	
Glu	Ser	Gly	Ala	Pro	Cys	Gln	Arg	Trp	Asp	Ser	Gln	Thr	Pro	His	Arg
			20					25					30		
His	Ser	Lys	Tyr	Thr	Pro	Glu	Arg	Tyr	Pro	Ala	Lys	Gly	Leu	Gly	Glu
		35					40					45			
Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Glu	Arg	Pro	Trp	Cys	Tyr	Thr
	50					55					60				
Thr	Asp	Pro	Arg	Val	Arg	Trp	Glu	Tyr	Cys	Asp	Ile	Pro	Arg	Cys	
65					70					75					

<210> 86  
 <211> 83  
 <212> PRT  
 <213> Artificial Sequence

<220>



<223> Description of Artificial Sequence: Kringle domain  
Consensus Sequence

<400> 86

Arg	Asp	Cys	Tyr	Ala	Gly	Asn	Gly	Glu	Ser	Tyr	Arg	Gly	Thr	Ala	Ser
1				5					10					15	
Thr	Thr	Lys	Ser	Gly	Lys	Pro	Cys	Gln	Arg	Trp	Asp	Ser	Gln	Thr	Pro
			20					25					30		
His	Leu	His	Arg	Phe	Thr	Pro	Glu	Arg	Phe	Pro	Glu	Leu	Gly	Leu	Glu
		35					40					45			
His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ser	Glu	Gly	Pro	Trp	Cys
	50					55					60				
Tyr	Thr	Thr	Asp	Pro	Asn	Val	Arg	Trp	Glu	Tyr	Cys	Asp	Ile	Pro	Gln
65					70					75					80
Cys Glu Ser															

<210> 87

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin-like  
serine protease Consensus Sequence

<400> 87

Arg	Ile	Val	Gly	Gly	Ser	Glu	Ala	Asn	Ile	Gly	Ser	Phe	Pro	Trp	Gln
1				5					10					15	
Val	Ser	Leu	Gln	Tyr	Arg	Gly	Gly	Arg	His	Phe	Cys	Gly	Gly	Ser	Leu
			20					25					30		
Ile	Ser	Pro	Arg	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Val	Tyr	Gly	Ser
		35					40					45			
Ala	Pro	Ser	Ser	Ile	Arg	Val	Arg	Leu	Gly	Ser	His	Asp	Leu	Ser	Ser
	50					55					60				
Gly	Glu	Glu	Thr	Gln	Thr	Val	Lys	Val	Ser	Lys	Val	Ile	Val	His	Pro
65					70					75					80

Cura 468 SEQ list 0405.txt

Asn	Tyr	Asn	Pro	Ser	Thr	Tyr	Asp	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Leu
				85					90					95	
Ser	Glu	Pro	Val	Thr	Leu	Ser	Asp	Thr	Val	Arg	Pro	Ile	Cys	Leu	Pro
			100					105					110		
Ser	Ser	Gly	Tyr	Asn	Val	Pro	Ala	Gly	Thr	Thr	Cys	Thr	Val	Ser	Gly
		115					120					125			
Trp	Gly	Arg	Thr	Ser	Glu	Ser	Ser	Gly	Ser	Leu	Pro	Asp	Thr	Leu	Gln
	130					135					140				
Glu	Val	Asn	Val	Pro	Ile	Val	Ser	Asn	Ala	Thr	Cys	Arg	Arg	Ala	Tyr
145					150					155					160
Ser	Gly	Gly	Pro	Ala	Ile	Thr	Asp	Asn	Met	Leu	Cys	Ala	Gly	Gly	Leu
				165					170					175	
Glu	Gly	Gly	Lys	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val
			180					185					190		
Cys	Asn	Asp	Pro	Arg	Trp	Val	Leu	Val	Gly	Ile	Val	Ser	Trp	Gly	Ser
		195					200					205			
Tyr	Gly	Cys	Ala	Arg	Pro	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser
	210					215					220				
Ser	Tyr	Leu	Asp	Trp	Ile										
225					230										

<210> 88

<211> 217

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin  
Consensus Sequence

<400> 88

Ile	Val	Gly	Gly	Arg	Glu	Ala	Gln	Ala	Gly	Ser	Phe	Pro	Trp	Gln	Val
1				5					10					15	

Ser	Leu	Gln	Val	Ser	Ser	Gly	His	Phe	Cys	Gly	Gly	Ser	Leu	Ile	Ser
			20					25					30		

Glu	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Val	Ser	Gly	Ala	Ser	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Cura 468 SEQ list 0405.txt

35

40

45

Val	Arg	Val	Val	Leu	Gly	Glu	His	Asn	Leu	Gly	Thr	Thr	Glu	Gly	Thr
	50					55					60				
Glu	Gln	Lys	Phe	Asp	Val	Lys	Lys	Ile	Ile	Val	His	Pro	Asn	Tyr	Asn
65					70					75					80
Pro	Asp	Thr	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Leu	Lys	Ser	Pro	Val	Thr
				85					90					95	
Leu	Gly	Asp	Thr	Val	Arg	Pro	Ile	Cys	Leu	Pro	Ser	Ala	Ser	Ser	Asp
			100					105					110		
Leu	Pro	Val	Gly	Thr	Thr	Cys	Ser	Val	Ser	Gly	Trp	Gly	Arg	Thr	Lys
		115					120					125			
Asn	Leu	Gly	Thr	Ser	Asp	Thr	Leu	Gln	Glu	Val	Val	Val	Pro	Ile	Val
	130					135						140			
Ser	Arg	Glu	Thr	Cys	Arg	Ser	Ala	Tyr	Gly	Gly	Thr	Val	Thr	Asp	Thr
145					150					155					160
Met	Ile	Cys	Ala	Gly	Ala	Leu	Gly	Gly	Lys	Asp	Ala	Cys	Gln	Gly	Asp
				165					170					175	
Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Asp	Gly	Glu	Leu	Val	Gly	Ile	Val
			180					185					190		
Ser	Trp	Gly	Tyr	Gly	Cys	Ala	Val	Gly	Asn	Tyr	Pro	Gly	Val	Tyr	Thr
		195					200					205			
Arg	Val	Ser	Arg	Tyr	Leu	Asp	Trp	Ile							
	210					215									

<210> 89

<211> 79

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Divergent  
subfamily of APPLE domains Consensus Sequence

<400> 89

Lys	Ser	Asp	Asp	Cys	Phe	Val	Arg	Leu	Pro	Asn	Thr	Lys	Leu	Pro	Asp
1				5					10					15	

Cura 468 SEQ list 0405.txt

Phe Ser Pro Ile Val Ile Ser Val Ala Ser Leu Glu Glu Cys Ala Gln  
20 25 30

Lys Cys Leu Asn Ser Asn Cys Ser Cys Arg Ser Phe Thr Tyr Asn Asn  
35 40 45

Asp Thr Lys Gly Cys Leu Leu Trp Ser Glu Ser Ser Leu Gly Asp Ala  
50 55 60

Arg Gln Leu Leu Pro Ser Gly Gly Val Asp Tyr Tyr Glu Lys Ile  
65 70 75

<210> 90

<211> 145

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Lipocalin/cytosolic fatty-acid binding protein  
family Consensus Sequence

<400> 90

Lys Phe Ala Gly Lys Trp Tyr Leu Val Ala Ser Ala Asn Phe Asp Pro  
1 5 10 15

Glu Leu Lys Glu Glu Leu Gly Val Leu Glu Ala Thr Arg Lys Glu Ile  
20 25 30

Thr Pro Leu Lys Glu Gly Asn Leu Glu Ile Val Phe Asp Gly Asp Lys  
35 40 45

Asn Gly Ile Cys Glu Glu Thr Phe Gly Lys Leu Glu Lys Thr Lys Lys  
50 55 60

Leu Gly Val Glu Phe Asp Tyr Tyr Thr Gly Asp Asn Arg Phe Val Val  
65 70 75 80

Leu Asp Thr Asp Tyr Asp Asn Tyr Leu Leu Val Cys Val Gln Lys Gly  
85 90 95

Asp Gly Asn Glu Thr Ser Arg Thr Ala Glu Leu Tyr Gly Arg Thr Pro  
100 105 110

Glu Leu Ser Pro Glu Ala Leu Glu Leu Phe Glu Thr Ala Thr Lys Glu  
115 120 125

Cura 468 SEQ list 0405.txt

Leu Gly Ile Pro Glu Asp Asn Val Val Cys Thr Arg Gln Thr Glu Arg  
130 135 140

Cys  
145

<210> 91  
<211> 218  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Connexin  
Consensus Sequence

<400> 91

Met Asp Trp Ser Phe Leu Gly Arg Leu Leu Glu Gly Val Asn Lys His  
1 5 10 15

Ser Thr Ala Ile Gly Lys Ile Trp Leu Ser Val Leu Phe Ile Phe Arg  
20 25 30

Ile Leu Val Leu Gly Val Ala Ala Glu Ser Val Trp Gly Asp Glu Gln  
35 40 45

Ser Asp Phe Val Cys Asn Thr Gln Gln Pro Gly Cys Glu Asn Val Cys  
50 55 60

Tyr Asp Gln Phe Phe Pro Ile Ser His Val Arg Leu Trp Val Leu Gln  
65 70 75 80

Leu Ile Phe Val Ser Thr Pro Ser Leu Leu Tyr Leu Gly His Val Ala  
85 90 95

Tyr Arg Val Arg Arg Glu Glu Lys Leu Arg Glu Lys Glu Glu Glu His  
100 105 110

Ser Lys Gly Leu Tyr Ser Glu Glu Ala Lys Lys Arg Cys Gly Ser Glu  
115 120 125

Asp Gly Lys Val Arg Ile Arg Gly Gly Leu Trp Trp Thr Tyr Val Phe  
130 135 140

Ser Ile Ile Phe Lys Ser Ile Phe Glu Val Gly Phe Leu Tyr Gly Gln  
145 150 155 160

Cura 468 SEQ list 0405.txt

Tyr Leu Leu Tyr Gly Phe Thr Met Ser Pro Leu Val Val Cys Ser Arg  
165 170 175

Ala Pro Cys Pro His Thr Val Asp Cys Phe Val Ser Arg Pro Thr Glu  
180 185 190

Lys Thr Ile Phe Ile Val Phe Met Leu Val Val Ser Ala Ile Cys Leu  
195 200 205

Leu Leu Asn Leu Ala Glu Leu Phe Tyr Leu  
210 215

<210> 92

<211> 59

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Src homology 3  
domains Consensus Sequence

<400> 92

Glu Gly Pro Gln Val Arg Ala Leu Tyr Asp Tyr Thr Ala Gln Asp Pro  
1 5 10 15

Asp Glu Leu Ser Phe Lys Lys Gly Asp Ile Ile Thr Val Leu Glu Lys  
20 25 30

Ser Asp Asp Gly Trp Trp Lys Gly Arg Leu Gly Thr Gly Lys Glu Gly  
35 40 45

Leu Phe Pro Ser Asn Tyr Val Glu Glu Ile Asp  
50 55

<210> 93

<211> 57

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SH3 domain  
Consensus Sequence

<400> 93

Pro Lys Val Val Ala Leu Tyr Asp Tyr Gln Ala Arg Glu Ser Asp Glu  
1 5 10 15

Cura 468 SEQ list 0405.txt

Leu Ser Phe Lys Lys Gly Asp Ile Ile Ile Val Leu Glu Lys Ser Asp  
20 25 30  
Asp Gly Gly Trp Trp Lys Gly Arg Leu Lys Gly Thr Lys Glu Gly Leu  
35 40 45  
Ile Pro Ser Asn Tyr Val Glu Pro Val  
50 55

<210> 94  
<211> 91  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fes/CIP4  
homology domain Consensus Sequence

<400> 94  
Met Gly Phe Trp Ser Glu Leu Asp Asp Gly Phe Glu Ala Leu Leu Ser  
1 5 10 15  
Arg Leu Lys Asn Gly Leu Arg Leu Leu Glu Asp Leu Lys Lys Phe Met  
20 25 30  
Arg Glu Arg Ala Lys Ile Glu Glu Glu Tyr Ala Lys Lys Leu Gln Lys  
35 40 45  
Leu Ser Lys Lys Leu Arg Ala Val Arg Asp Thr Glu Ser Glu Leu Gly  
50 55 60  
Ser Leu Arg Lys Ala Trp Glu Val Leu Leu Ser Glu Thr Asp Ala Leu  
65 70 75 80  
Ala Lys Gln His Leu Gln Leu Ser Glu Asp Leu  
85 90

<210> 95  
<211> 94  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Fes/CIP4  
homology domain Consensus Sequence

Cura 468 SEQ list 0405.txt

<400> 95

Met	Gly	Phe	Gly	Ser	Glu	Leu	Cys	Pro	Glu	Gly	His	Lys	Ala	Leu	Leu
1				5					10					15	
Ser	Arg	Gln	Asp	Asn	Glu	Leu	Arg	Leu	Leu	Glu	Glu	Met	Lys	Lys	Phe
			20					25					30		
Met	Ala	Glu	Arg	Ala	Lys	Ile	Glu	Lys	Glu	Tyr	Ala	Gly	Lys	Leu	Gln
		35					40					45			
His	Leu	Ser	Ala	Gln	Val	Gly	Lys	Gly	Pro	Ala	Thr	Ala	Glu	Gly	Glu
	50					55					60				
Asp	Glu	Leu	Ser	Ser	Leu	Lys	Ser	Trp	Ala	Val	Ile	Leu	Ser	Glu	Thr
65					70					75					80
Glu	Gln	Gln	Ser	Lys	Ile	His	Leu	Gln	Ile	Ser	Glu	Asp	Leu		
				85					90						

<210> 96

<211> 230

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Trypsin-like  
serine protease Consensus Sequence

<400> 96

Arg	Ile	Val	Gly	Gly	Ser	Glu	Ala	Asn	Ile	Gly	Ser	Phe	Pro	Trp	Gln
1				5					10					15	
Val	Ser	Leu	Gln	Tyr	Arg	Gly	Gly	Arg	His	Phe	Cys	Gly	Gly	Ser	Leu
			20					25					30		
Ile	Ser	Pro	Arg	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Val	Tyr	Gly	Ser
		35					40					45			
Ala	Pro	Ser	Ser	Ile	Arg	Val	Arg	Leu	Gly	Ser	His	Asp	Leu	Ser	Ser
	50					55					60				
Gly	Glu	Glu	Thr	Gln	Thr	Val	Lys	Val	Ser	Lys	Val	Ile	Val	His	Pro
65					70					75					80
Asn	Tyr	Asn	Pro	Ser	Thr	Tyr	Asp	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Leu
				85					90					95	



Cura 468 SEQ list 0405.txt

Ser	Glu	Pro	Val	Thr	Leu	Ser	Asp	Thr	Val	Arg	Pro	Ile	Cys	Leu	Pro
			100					105					110		
Ser	Ser	Gly	Tyr	Asn	Val	Pro	Ala	Gly	Thr	Thr	Cys	Thr	Val	Ser	Gly
		115					120					125			
Trp	Gly	Arg	Thr	Ser	Glu	Ser	Ser	Gly	Ser	Leu	Pro	Asp	Thr	Leu	Gln
	130					135					140				
Glu	Val	Asn	Val	Pro	Ile	Val	Ser	Asn	Ala	Thr	Cys	Arg	Arg	Ala	Tyr
145					150					155					160
Ser	Gly	Gly	Pro	Ala	Ile	Thr	Asp	Asn	Met	Leu	Cys	Ala	Gly	Gly	Leu
				165					170					175	
Glu	Gly	Gly	Lys	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val
			180					185					190		
Cys	Asn	Asp	Pro	Arg	Trp	Val	Leu	Val	Gly	Ile	Val	Ser	Trp	Gly	Ser
		195					200					205			
Tyr	Gly	Cys	Ala	Arg	Pro	Asn	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser
	210					215					220				
Ser	Tyr	Leu	Asp	Trp	Ile										
225					230										

<210> 97  
 <211> 217  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Trypsin  
 Consensus Sequence

<400> 97															
Ile	Val	Gly	Gly	Arg	Glu	Ala	Gln	Ala	Gly	Ser	Phe	Pro	Trp	Gln	Val
1				5					10					15	
Ser	Leu	Gln	Val	Ser	Ser	Gly	His	Phe	Cys	Gly	Gly	Ser	Leu	Ile	Ser
			20					25					30		
Glu	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Val	Ser	Gly	Ala	Ser	Ser
		35					40					45			

Cura 468 SEQ list 0405.txt

Val	Arg	Val	Val	Leu	Gly	Glu	His	Asn	Leu	Gly	Thr	Thr	Glu	Gly	Thr
50						55					60				
Glu	Gln	Lys	Phe	Asp	Val	Lys	Lys	Ile	Ile	Val	His	Pro	Asn	Tyr	Asn
65					70					75					80
Pro	Asp	Thr	Asn	Asp	Ile	Ala	Leu	Leu	Lys	Leu	Lys	Ser	Pro	Val	Thr
				85					90					95	
Leu	Gly	Asp	Thr	Val	Arg	Pro	Ile	Cys	Leu	Pro	Ser	Ala	Ser	Ser	Asp
			100					105					110		
Leu	Pro	Val	Gly	Thr	Thr	Cys	Ser	Val	Ser	Gly	Trp	Gly	Arg	Thr	Lys
		115					120					125			
Asn	Leu	Gly	Thr	Ser	Asp	Thr	Leu	Gln	Glu	Val	Val	Val	Pro	Ile	Val
		130				135						140			
Ser	Arg	Glu	Thr	Cys	Arg	Ser	Ala	Tyr	Gly	Gly	Thr	Val	Thr	Asp	Thr
145					150					155					160
Met	Ile	Cys	Ala	Gly	Ala	Leu	Gly	Gly	Lys	Asp	Ala	Cys	Gln	Gly	Asp
				165					170					175	
Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Asp	Gly	Glu	Leu	Val	Gly	Ile	Val
			180					185					190		
Ser	Trp	Gly	Tyr	Gly	Cys	Ala	Val	Gly	Asn	Tyr	Pro	Gly	Val	Tyr	Thr
		195					200					205			
Arg	Val	Ser	Arg	Tyr	Leu	Asp	Trp	Ile							
		210				215									

<210> 98

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: NOV5 Primer 1

<400> 98

ctcccactcc tgctgcttct gact

24

<210> 99

Cura 468 SEQ list 0405.txt

<211> 25  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: NOV5 Primer 2  
  
<400> 99  
aaggctgggc ctaacccagt ctcac 25

<210> 100  
<211> 23  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: NOV7 Primer 1  
  
<400> 100  
catgaactgg gcatttctgc agg 23

<210> 101  
<211> 27  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: NOV7 Primer 2  
  
<400> 101  
ttatctgctg atctcgcagg ttatgga 27

<210> 102  
<211> 22  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: NOV8 Primer 1  
  
<400> 102  
ctgacaggcc ctggtgtgtg at 22

<210> 103  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NOV8 Primer 2

<400> 103  
tcacacatgt ttcatgtggg agttaga 27

<210> 104  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NOV9 Primer 1

<400> 104  
gagtgagagg tcggacagac tgtg 24

<210> 105  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NOV9 Primer 2

<400> 105  
actcatgcaa cttgcttctc tcactct 27

<210> 106  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: NOV10b Primer  
1

<400> 106  
cctatgagcc tgatgctgga tgac 24

<210> 107  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: NOV10b Primer  
2

<400> 107  
aggactcaga ggaggagtc ctgag 25

<210> 108  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag4164 Forward

<400> 108  
gcactacaag tggaagcctt ac 22

<210> 109  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag4164 Probe

<400> 109  
ctcaagtaga agccgactta tgcaaa 26

Cura 468 SEQ list 0405.txt

<210> 110  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag4164 Reverse

<400> 110  
tcaaatcctt ctgcgatata gt 22

<210> 111  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1313b  
Forward

<400> 111  
cagctgcacg attaatgaag at 22

<210> 112  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1313b Probe

<400> 112  
aggtcttgga ctggccttca ccatt 25

<210> 113  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1313b  
Reverse

<400> 113  
ccaaagttgt gtccagactc at 22

<210> 114  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2197 Forward

<400> 114  
ccaaggaaga cctcttcatc tt 22

<210> 115  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2197 Probe

<400> 115  
tcttgcttac ggcataagcg ctctct 26

<210> 116  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2197 Reverse

<400> 116  
ttcatttcta tgggacctca ga 22

<210> 117  
<211> 21  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag708 Forward

<400> 117

aaagatggga ctcgtcatga c

21

<210> 118

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag708 Probe

<400> 118

cacgccatct tactgactgg tctgga

26

<210> 119

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag708 Reverse

<400> 119

gtgcaaattcc caaagtgtca

20

<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag4164 Forward

<400> 120

gcactacaag tggaagcctt ac

22



Cura 468 SEQ list 0405.txt

<210> 121  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag4164 Probe

<400> 121  
ctcaagtaga agccgactta tgcaaa

26

<210> 122  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag4164 Reverse

<400> 122  
tcaaatcctt ctgcgataca gt

22

<210> 123  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag2197 Forward

<400> 123  
ccaaggaaga cctcttcatc tt

22

<210> 124  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag2197 Probe

Cura 468 SEQ list 0405.txt

<400> 124  
tcttgcttac ggcataagcg ctctct 26

<210> 125  
<211> 22  
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<220>  
<223> Description of Artificial Sequence: Ag2197 Reverse

<400> 125  
ttcatttcta tgggacctca ga 22

<210> 126  
<211> 22  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Ag2197 Forward

<400> 126  
ccaaggaaga cctcttcatc tt 22

<210> 127  
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<220>  
<223> Description of Artificial Sequence: Ag2197 Probe

<400> 127  
tcttgcttac ggcataagcg ctctct 26

<210> 128  
<211> 22  
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<213> Artificial Sequence

Cura 468 SEQ list 0405.txt

<220>

<223> Description of Artificial Sequence: Ag2197 Reverse

<400> 128

ttcatttcta tgggacctca ga

22

<210> 129

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag708 Forward

<400> 129

aaagatggga ctcgatcatga c

21

<210> 130

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag708 Probe

<400> 130

cacgccatct tactgactgg tctgga

26

<210> 131

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag708 Reverse

<400> 131

gtgcaaattcc caaagtgatca

20

Cura 468 SEQ list 0405.txt

<210> 132  
<211> 22  
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<220>  
<223> Description of Artificial Sequence: Ag1313b  
Forward

<400> 132  
cagctgcacg attaatagaag at 22

<210> 133  
<211> 25  
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<220>  
<223> Description of Artificial Sequence: Ag1313b Probe

<400> 133  
aggtcttgga ctggccttca ccatt 25

<210> 134  
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<220>  
<223> Description of Artificial Sequence: Ag1313b  
Reverse

<400> 134  
ccaaagttgt gtccagactc at 22

<210> 135  
<211> 22  
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<220>  
<223> Description of Artificial Sequence: Ag1537 Forward

<400> 135  
tttcaagaca ccctgtgata cc 22

<210> 136  
<211> 26  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Ag1537 Probe

<400> 136  
acttcgtgtc ctgaatgttc caggct 26

<210> 137  
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<220>  
<223> Description of Artificial Sequence: Ag1537 Reverse

<400> 137  
cagaggaatg aaggcataga tg 22

<210> 138  
<211> 21  
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<220>  
<223> Description of Artificial Sequence: Ag2432 Forward

<400> 138  
gtaggcaaag ggactcactg t 21

<210> 139  
<211> 26  
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag2432 Probe

<400> 139

cagaaatcaa taatcttttga ctgccg

26

<210> 140

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag2432 Reverse

<400> 140

gcacattacg tggctgaga

19

<210> 141

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag1250 Forward

<400> 141

cgtggtgaac tctgccttat at

22

<210> 142

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag1250 Probe

<400> 142

cacagagctg tcgtcttttga ccgatt

26

<210> 143  
<211> 21  
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<220>  
<223> Description of Artificial Sequence: Ag1250 Reverse

<400> 143  
agtccctttg cctaccacaa t 21

<210> 144  
<211> 20  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Ag3086 Forward

<400> 144  
ggacccatt cgactactgt 20

<210> 145  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag3086 Probe

<400> 145  
ctgatgacca gccgcatca atc 23

<210> 146  
<211> 20  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Ag3086 Reverse

<400> 146  
ttctcaaact gcacctggtc 20

<210> 147  
<211> 20  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Ag3797 Forward

<400> 147  
tctggacgac aactattgcc 20

<210> 148  
<211> 25  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Ag3797 Probe

<400> 148  
atggtgctac actacggatc cgcag 25

<210> 149  
<211> 20  
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<220>  
<223> Description of Artificial Sequence: Ag3797 Reverse

<400> 149  
gtcacagaat tctcgctcga 20

<210> 150  
<211> 22  
<212> DNA  
<213> Artificial Sequence



<220>

<223> Description of Artificial Sequence: Ag2439 Forward

<400> 150

tatcatcact tgtgatggca aa

22

<210> 151

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag2439 Probe

<400> 151

aaaaccgaga gcactttgaa aacaca

26

<210> 152

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag2439 Reverse

<400> 152

aaacttctct cccagggtac aa

22

<210> 153

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag2771 Forward

<400> 153

tgaacagaac tatgcgaaac aa

22

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<210> 154  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2771 Probe

<400> 154  
tctggttaag aagtactgcc ccaaacg 27

<210> 155  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag2771 Reverse

<400> 155  
ggctcttcat ctttggatga a 21

<210> 156  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1674 Forward

<400> 156  
ctcactcacc acaaggagat aa 22

<210> 157  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Ag1674 Probe

<400> 157

tgacatcaaa ctcaacagtt cccagga

27

<210> 158

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Ag1674 Reverse

<400> 158

gtctaggaga gagctgagca aa

22

<210> 159

<211> 78

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PAN domain  
Consensus Sequence

<400> 159

Cys	Ser	Ser	Phe	Val	Arg	Val	Pro	Gly	Arg	Ser	Leu	Ser	Gly	Asn	Asp
1				5				10						15	

Ile	Ser	Val	Val	Asn	Val	Pro	Ser	Leu	Glu	Glu	Cys	Ala	Ala	Leu	Cys
			20					25					30		

Leu	Glu	Glu	Pro	Arg	Val	Cys	Arg	Ser	Phe	Thr	Tyr	Asn	Asn	Lys	Ser
		35				40						45			

Lys	Gln	Cys	Leu	Leu	Lys	Ser	Glu	Ser	Ser	Gly	Ser	Leu	Pro	Arg	Leu
	50					55					60				

Lys	Arg	Pro	Ser	Gln	Lys	Val	Asp	Tyr	Tyr	Glu	Lys	Ser	Cys
65					70					75			

<210> 160

<211> 34

<212> PRT

<213> Artificial Sequence

Cura 468 SEQ list 0405.txt

<220>

<223> Description of Artificial Sequence: Connexin  
homologues Consensus Sequence

<400> 160

Ser Val Trp Gly Asp Glu Gln Ser Asp Phe Thr Cys Asn Thr Gln Gln  
1 5 10 15

Pro Gly Cys Glu Asn Val Cys Tyr Asp Gln Phe Phe Pro Ile Ser His  
20 25 30

Val Arg

<210> 161

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Zinc Metalloprotease  
conserved domain

<400> 161

Asn Glu Gln Lys  
1

<210> 162

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Zinc Metalloprotease  
conserved domain

<400> 162

Asn His Gln Lys  
1

<210> 163

<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Zinc Metalloprotease  
conserved domain

<400> 163

Asn Asp Glu Gln  
1

<210> 164  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Zinc Metalloprotease  
conserved domain

<400> 164

Gln His Arg Lys  
1

<210> 165  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Zinc Metalloprotease  
conserved domain

<400> 165

Met Ile Leu Val  
1

<210> 166  
<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Zinc Metalloprotease  
conserved domain

<400> 166

Met Ile Leu Phe

1